



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :

C12Q 1/68

A2

(11) International Publication Number:

WO 98/20165

(43) International Publication Date:

14 May 1998 (14.05.98)

(21) International Application Number: PCT/US97/20313

(22) International Filing Date: 5 November 1997 (05.11.97)

(30) Priority Data:

60/030,455

6 November 1996 (06.11.96)

US

(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published

*Without international search report and to be republished upon receipt of that report.*

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(54) Title: BIALLELIC MARKERS

(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION  
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,



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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

#### B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays; some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

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### 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

### 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

### III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(AA) = x^2$   
 Homozygote:  $p(BB) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$   
 Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

15 The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

20 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25 
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $\text{cum } p(ID)$ ) for each of multiple unlinked loci is determined by multiplying  
 30 the probabilities provided by each locus.

$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$



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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ), ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the



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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is  
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene  
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating  
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292  
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTC
						GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTGGAGCCAATCTTTATTT
						GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGGAGATAATGT
WI-7070	226	CT	---		---	TACTAGACTTTATGCCATGGTGCTTTCTAGITTAATGCTGTGCTCTGTGCTG
						AAGCCATTGACGTAACTCTCAGAGGTTATTGCGATGGATTGACTCTGGGACAAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT
						GATAATACATAAGCCCTAGGATTAGATACAATCTTGAAAGAACTGAGACAGATAATTCTGAATT
WI-10744	61	GC	---		---	AAATGAGGTAAAGTTTCAGGCACCTCA
						GGGCAATTACCAGCAAAAAGTCAAAATTACCAGCATCAAAAGTCAGGTGCAAAAGGAGGTAGAACAA
						TTACAGTAACATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAAATA[C/T]AGTG
						GGTCCCTAATAGTTATTAGTCCCTTTTCTCCCTCTTCTCAATCTCTGAATTTATTTTATACTTAA
WI-9975	126	CT	---		---	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATTTACTGAA
						GCTAGGTTTGTCTGTGGCTGTCTTCACTAGACTTGAGATGACTTGATTACAGTATCCCTATGT
						GATGTAACACTAGCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGTTTCAGAAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTCATCCTGTATTAAITTTCTCCCATATTAAITCAAAGGGAGTGGACAGGT
WI-8010	247	GT	---		---	CCCTGGCTGAAAAGAAATAAAGATCCCCAAAGTGGTGGGG[G/T]CTT
						GCCGGCCTATCTTTAATTTAACTTGTATCTTTGGTGTCTTCCATCTAGGATTCGCTTATAAT
						CTTTGTCTGTCTGT[G/C]ATTACCTGATCTACTTTTGTACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	GC	---		---	TCTCGACTCTATAACAACACTCCAACAGAA
						GCCCGCCTATCTTTAATTTAACTTGTATCTTTGGTGTCTTCCATCTA[G/C]GATTCTGCCTTAT
						AATCTTTGTCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	GC	---		---	TCTCGACTCTATAACAACACTCCAACAGAA
						TATGCACCTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAATGTATAAAAATAA
						ATATGTTATTATAGGCATTTATTACTAAGTATAGTCTTCTTGGAAAGGAACACCCAAACCAATACTT
						ATAAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTTCTCACA
WI-8007	242	CA	---		---	GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[G/C]AAGCTGCTG
						TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTTTGTAG
						TCTATATTCACACATATGAGTGAATTTCTGTTGGGCGATGGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAGAATTCCTTTGTTTAC
WI-9823	97	CT	---		---	ATGCTTTCCAACTGATTTGTATGACTATTGTATGCACAGTTGGATCACC



WI-9651b	105 A T ---	---	TCTACATTCTATGGACAACTCCATGCCCTTTCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGCTCATGTACAATTTCTGCTGCTCTTCA/TJGGGGCAGCTTGAAGCCTCCCTTTAGAC ACCTTACAGGTACAGCCACCATGCCCTACCTCCTCATGGCACTGCCAGGGACCCCTTATAGGCCTCTG TCTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGTCCTC
WI-9651	139 T C ---	---	TCTACATTCTATGGACAACTCCATGCCCTTTCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGCTCATGTACAATTTCTGCTGCTCTTCAAGGGCAGCTTGAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCCACCATGCCCTACCTCCTCATGGCACTGCCAGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGTCCTC
WI-7676b	309 A C ---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCTGCTATTTATTTTG TATTTATGCTTAATCTCTTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCGGCTCTCTTGGTGGCTGCTGGTGGTGGAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGTGC TCCCCCGTCTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCTGCTATTTATTTTG TATTTATGCTTAATCTCTTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC/TJGGCTCTCTTGGTGGCTGCTGGTGGTGGAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGTCTGTTCACTTCTCTCTCCTCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGAGTTTGAATATTTTGTG/TJGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTCTTTGTTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAATATCTTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATAGGGAAAATAAGACAATTTGA/T/A,CJGTACCCCGAGGAACAAGAG CCCTGCACCTTGAACCTCAAGAGTTCTATTTCTGGCTGTTCCAGACTTATTTGATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAAT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCTTCAAGAGCTGAAAAGGGTCCCTCGGCTTTTATTT CAGGGCTTGCATGGCTCTATTCCCTCTGCTCTC/CJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGAACAAGCTCATTGTACAGTGTCTGTTCATGAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGATCACCACACTCAATAATATCACTTATGTGCTATCAGATATCCTCTCT ACCCTCAGCTTATTTGAAGAAAATCCTAAACATCAATCTTTCATCCATAAAAATGTACGATTT /CJATTAATAAACATAACTTTTAAAGAAAACATAGGACACATTTTCAAAATTAATAAAAATAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTATCATGCTAG

WI-10826	132 A C ---	---	TCCTATTGCAATTCACAGTAGCCCATGAAGTAGGTAAACAGCCTCTATTTAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTCTCTAATAAGCAAGACCTGCAJ/C JCCCTGGCTCTGACTCCAAAGCTTATCCCTTCATGCTGTTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACTTTGGAGATTCAATTTCTTGAGTGGCACTGCAT GCTCATTCAAGTGAACACTTTGGGGTATAGAAATGGAATGGAGAGTTTCAACACAGCTTTGCTGAAAC TGACTTTGGGJAJCTCCAGACTTCACTGCTTAGGCATTGAACCATCACCTGGTTTGCAATCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACACAGAATCATCAAGGACJAJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTTCTATGGAACCTCTCCGACTCTGTAATTTTCAATTTCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCAGTAAAGCAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAGGGCAGCTTGTGCGAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATATGGGCTAGTGTCTTTGGGTTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAG TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATATGGGCTAGTGTCTTTGGGTTGAGCGGATT ATGJAJCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAG TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACAGCCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCTGJAJCTGCAGAGTATAGGACCGGTTCCAACTTT
WI-9484	178 G A ---	---	TCAACAGCCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGACAGGJAJAGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGACCGGTTCCAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTTGGGCATATAGGTTT GTGACACAGAAGTCTACTTTGGTGGCTAAAGTTTACTAAGGAAAATAACTGAAAAGATTAAAG TGAGAGTCJTJGAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG
WI-9443	211	G A	---	---	TTAAAAACAGTTTCAGGTTGGTGAAGCAGAAAAGGATGTGATTACAATTTAAATGAATCAGTCACCT GCACAAATTAATCTCTTGGCATCATACAAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAAGGCACCTGCACCCA CTGACGAGACGACGACAGACCTTGGACTACAGATGACACACATGCCACCTT
WI-7166	59	C T	---	---	TCTCTCAAAAGAGAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TGGAT CATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTCATCTCTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGTGTTTAAACTTGTGCTGTGAACAAATGTGAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTCTGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGT/CJTGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188	G T	---	---	GCTTCTTCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTCTGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGT/CJTGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCTGTGGAGGTGGCAATTTAGTGTGACCTTGCAAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATAG GCCATAAAGTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGAACACTC TGGTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCCAACTTCCCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTCT/CJTCTTCTCCCTCTGGATCA AAGTAGGCAGGACCATTGGACCCAGGTCTTGGAGCTGAGCCCTCTCACCTGTACTCTTCCGAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCATGGCTTCTCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTGCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTTGTTATTTTAGAGGGTTTAACAATGGCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGAGGGCTCCCTG/A/CCTGTGATGCTACCTAACTGCTACTTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAGCTGAAATGAAATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTCTTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACGTGCTACTGTTGATGGATTTATAATTATTTGCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGATGGATTTATAATTATTTGCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGATGGATTTATAATTATTTGCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---	GGATGACTTACCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGAGTGGGATGGCAGA GACATCCACCTTAGCAAGTGGG[C/T]ACCTACTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGACG CTGAGCCACTCTTAAACCATGAACCATCAACATTTAAATAACGTTGCCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGAGTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGACCTACTTAGA[G/A]CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGACG CTGAGCCACTCTTAAACCATGAACCATCAACATTTAAATAACGTTGCCCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCATTTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATATCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCATTTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATATCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTGA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTCAGG TTAACAGCCACATTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCCTTATGCACCCAAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGTGGCACTCATGGAGGGG(C/G)TGCAGGTGGAACATATGCACTATGCACTGCTCCGGCCACACA TCCTGCTGGGCCCCCTACCCCTGCCCAATTCAATCCTGCCAATAAATCCTGTCTATTGTTGTCATCCTG GAGAAATTGAAGGGAGGTCAAGTTGTTGTCAATGATTGTGCAGAGAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCCTTGAGGAGCCGCCACCAAGTGTGAATCCCCATCCCATCTGT/CJGTATGAG TCCCAATTTGCCTTGCAATTAGCAATCTGTCTCCCCCAAAAAGAAATGTCTATGAAGCTTTCTTTCT ACACACTGTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTACGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCCATACAGCCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGGTCTGCCATGCTCTGG AGGACAAAGGGGCCACATCCCCACCCAGCTGTACCCAGCCCGGGCAGGTGCAGCCCTTCTCTCC TGCTCTG(C/A)CTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGTTGTTGCCCTCTG TGCTGCTCATCCATCCTCTTACTGGGGCTGGGGCTAGCCCCA
WI-4767b	173 C A ---	---	---	TTCCAGTCTGTTTATCCCTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA(C/A)AAATCACTAAGGAATTCACACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	---	TTCCAGTCTGTTTATCCCTTTCATTGTCAAAAAGATGCTCTTAGACTGA(C/A)ATTCATAAAGAGTT CCTCAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACACTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA(C/T)CATGCAGGAAGGAAACTATGTATTAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT/CJGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT

WI-7718c	91 C G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7718a	42 A T ---	C		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7227d	99 G C ---			AGGGAATTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---			AGGGAATTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACAGTG TTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---			AGGGAATTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---			AGGGAATTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---			CCCAATGCCCTCCACAGATGCAAGGACTCTGCTGCTCTGGAGGTGGAGACAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGATCCCTCATCGAACAACTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTCTATTGAACTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCTGCCCATCCCAACATGATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCCTCTCCACGATGTCAAGGACTCCTGTCTGCTGGAGGTGGGAGACAAAGGAACCTTAA JCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCTTCATCGAACAACACTGATCGGAA AACTTGAATCTGTACTGAAATGAGGAGAGAGACATGTCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTGTACACCTGCCCTGGGACTCCTATGATGGCTGCTGTTGATAATAATCA GATCATGCCCAAGAGCGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAATCGCTCC CTGAGGAGAAAATCTGGAGGAGCTG/GJGTGTGATGAAGGTGATGTTGGAGGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACCTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTGTACACCTGCCCTGGGACTCCTATGATGGCTGCTGTTGATAATAA TCAGATCATGCCCAAGAGCGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAATGC GTCCCTGAGGAGAAAATCTGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGAGGGAGCACAGTG TCTGTGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACCTA
WI-7381c	213 C T ---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGTTTCTGCCCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTC/GTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGTTTCTGCCCTATGGTGAG ATCAGATGTGGCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGTTTCTGCCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTCCGACCTTCATATTAATAAGAGCAATGAGAGCGGGAATAATTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCTGAAACAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTAGGTTTGTCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTCCGACCTTCATATTAATAAGAGCAATGAGAGCGGGAATAATTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GGATGTAGATTGTCACATTCAATCTGAAACAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTAGGTTTGTCC

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WI-1795b	130 TC ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTCCAGACTCCTACGATTAA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCAAGAAAGTTG/CJC GTCTACCAATTTACCAAATTCGTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 TC ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT/CJCTCCAGACTCCTACGA TTAAATGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCAAGAAAGAAAGTC GTCTACCAATTTACCAAATTCGTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 GA ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136 GA ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141 CT ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116 GC ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52 GA ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTG/GAJATAATAA AAACCCGTGAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA AATTTATTTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACCTTTTGGACTGTCCTTTATTTCT
WI-1126b	230 TC ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAATGCAATCCAGCTGTAACCTTTTTC/GGAGCTGTCCTTTATTTCT



WI-1126a	97 T C ---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAAACTCCAGTATCACTGATACATAATAAAAA CCCTGTAAAGTCTGCTTGCAATTTCAAGATT/CJCAATATATATCCAGATTGTTTCCAGCAAGAAAA ATTTTATTTCTCAAGATATAAAAAATAAATATTAAATTCAGTTTCCCAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124 C T ---			TAGTGCTAAATTTTGGAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGTATTAATTCAGATGTATTTTGGCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAGGATAGAGTTTAAAT/CJJA TTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAAATTTTGGAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGTATTAATTCAGATGTATTTTGGCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAGGATAGAGTTTAAAT/CJJA TTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAAATTTTGGAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGTATTAATTCAGATGTATTTTGGCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTTGCTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCTGCTCAGACCAATTTCTCTATCTGGAGGCTCTTCCCTTGACTTTCTCTG TTCACCAACCTTCTTTTATTCTCAGGACACTCA/GAJTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTCTTCC
WI-10770a	49 G T ---			GCTTGGTTTGCTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTCTG/JCCTGGCCCTTTTGATTT TCACCCATACCTCTATGCTGCTCAGACCAATTTCTCTATCTGGAGGCTCTTCCCTTGACTTTCTC CTGTTCCACCAACCTTCTTTTATTCTTCAGGACACTCAGTTCCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTCTTCC
WI-9667b	82 C T ---			GATGACAACTTCTGTGACCCCTTAGTCTTGCTCATGACACTTTTCAATCTCTGCCTTGATCATGG TTATCACTGGACA/CJTAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTCATAGGCATGGTAACTAAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT
WI-9667a	68 G C ---			GATGACAACTTCTGTGACCCCTTAGTCTTGCTCATGACACTTTTCAATCTCTGCCTTGATCATG G/CJTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTCATAGGCATGGTAACTAAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT

WI-10400d	189 A G ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTAAATTT TCCTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTAAATTT TCCTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCT GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTAAATTT TCCTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTA ATTTTCTTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTCACCACCTTAGAAAAGGGCATTTCAGACATTCATGAGGCTTCATATACTGGTTAG CAACAATGGATGTTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAAACTAAGGCCAAACCAATGAACCTGATAGGAGGGTAATGCAAGGGGAGAGA CCCCACCTCTCACCACCTTAGAAAAGGGCATTTCAGACATTCATGAGGCTTCATATACTGGTTAGC AAACAATGGATGTTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31 G A ---	---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGCG/AJCTCTCAGCTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATACTAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTGAGGAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64 G T ---	---	---	ATACGCTTCTGTCTGCCACAGTGGAAACAGCAACCCAGGTGGCCAGGGTCCGAGTCCACACA(G/T) CCCTCAGCCCTTCAGCTTTCATGTGTCATCGGTGACTCAGCAGACAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCCTCTCTGGAATTTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTTCTAAGCAACGACGGAGC
WI-3429a	62 C T ---	---	---	ATACGCTTCTGTCTGCCACAGTGGAAACAGCAACCCAGGTGGCCAGGGTCCGAGTCCACACA(C/T)AG CCCTCAGCCCTTCAGCTTTCATGTGTCATCGGTGACTCAGCAGACAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCCTCTCTGGAATTTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTTCTAAGCAACGACGGAGC
WI-6786c	151 G A ---	---	---	ATTTTAGGACAGTGAAAAAAGGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAAGTGAAGTGAAGTGA GTGAGCCCCATTCTT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786b	111 A T ---	---	---	ATTTTAGGACAGTGAAAAAAGGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAAGTGAAGTGAAGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786a	106 A T ---	---	---	ATTTTAGGACAGTGAAAAAAGGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAAGTGAAGTGAAGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6711b	226 G T ---	---	---	GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAGTATTGGGAAGAAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCTTAACCTTCACTTCCAACTCACTGAAT TTCATATACCTCCATTATTAATTCATATCATCATTCAGAGAGAAAGACACGGTGCCAACTGGGTT TGTTGGTGGCTGCACACCCACAGTGGCAACTAAGTGTAACTCTCTAAA
WI-6711a	36 T C ---	---	---	GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAGTATTGGGAAGAAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCTTAACCTTCACTTCCAACTCACT GAATTCATATACCTCCATTATTAATTCATATCATCATTCAGAGAGAAAGACACGGTGCCAACTG GGTTTGGTGGTGGCTGCACACCCACAGTGGCAACTAAGTGTAACTCTCTAAA

WI-10613b	172 A C ---	---	ATTTGATGCCAAATCATAATACCGTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAATATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTTT TTTGCAACTTTTGACAAGGCCAGGCAATTTTATTTGAC/GC/GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	ATTGTATGCCAAATCATAATACCGTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAATATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	GCCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTTCCAAACAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAAJA TJGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCCCTCT TTCCACATGCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81 G A ---	---	GCCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTTCCAAACAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCCCTCT TCCACATGCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28 C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTTCCAAACAGTGACTACCCCTTGA AGCATATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCCCTCT TCCACATGCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103 T A ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAGAGCCCTTAAAGACAGCCATTTTATCCTAATTGG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTTAAAG
WI-10681a	41 A T ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAGAGCCCTTAAAGACAGCCATTTTATCCTAATTGG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTTAAAG
WI-7222c	126 G T ---	---	GCCTCTCCTCAACTGTCTGGACCAAGGCTAGGAAAGGCTGTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTCTCAAGTTGGGGATGGG[G]TAATAA AGGAGGGGAATTCCTTGACAAGAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGATTTTCAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---		<p>GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTGGTCCCCCTTT  AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG  AGGGGGAATCCCTTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA  GACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTCTCA</p>
WI-7222a	126	G T ---	---		<p>GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTGGTCCCCCTTT  AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG[GT/AAATAA  AGGAGGGGAATCCCTTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTT  TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT</p>
WI-8054d	41	C A ---	---		<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT  CTTGATCTTTTAATAGCCAGGATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA  CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCTGCT  TCCTGTACATACGCCGCTTTCCCTGGGCGTACAGAGATCCTTGGCCCTT</p>
WI-8054c	237	G T ---	---		<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT  GCATCTTTTAATAGCCAGGATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA  TCTTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCTTCC  TGTCATAACGCCGCTTTCCCTGGGCGTACAGAG[GT/AAATCCTTGGCCCTT</p>
WI-8054b	148	T C ---	---		<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT  GCATCTTTTAATAGCCAGGATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA  TCTTCTTTGTAG[TC/TTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT  TCCTGTACATAACGCCGCTTTCCCTGGGCGTACAGAGATCCTTGGCCCTT</p>
WI-8054a	131	C G ---	---		<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT  GCATCTTTTAATAGCCAGGATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[CT/GJA  CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT  TCCTGTACATAACGCCGCTTTCCCTGGGCGTACAGAGATCCTTGGCCCTT</p>
WI-10854b	152	G T ---	---		<p>TTCCACAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA  ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAGACGATAGTTAACGCTCTGGTAAGTTTAT  ACGGTGTGCGAGGCAACA[GT/GGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTTCTTG  TTTTAGACACAGGGTCTGCTGTGTG</p>
WI-10854a	102	C T ---	---		<p>TTCCACAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA  ATGTTTATATTTACTTTAAAGCGAAGTTGAACAC[CT/GAAGACGATAGTTAACGCTCTGGTAAGTT  TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTTCTTG  TTTTAGACACAGGGTCTGCTGTGTG</p>

WI-9826b	127	G A ---	---	---	AATTTATATGTGAAGGTTAGCAAACATATGCCACAGGCCCATCTAGCCATGCCCTATTTTGTG TGCCTGATGGCTGTTGGTGTTTGCACGAGTTAGCCATTGTGACAGAGGCTGTATG/AJGCCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTGAAGGTTAGCAAACATATGCCACAGGCCCATCTAGCCATGCCCTATTTTGTG TGCCTGATGGCTGTTGGTGTTTGCACGAGTTAGCCATTGTGACAGAGGCTGT/AJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTTGAA
WI-15986	60	T G GTGGTTTTT	TTTGTGTGT AAACGTAAAA GAAATGT	TGACATTATAT	CGGACACGTGTATATACAAATACAGATCGTATGGTTTGTGTGTGGTTTTTTTTTTT/GJTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G A G	AACTGCAAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAAGTAACGTCAAATAGGAAACCAGAG/AJGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTAT
WI-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGAGAGATTACAAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAAGA
WI-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGAGAGATTACAAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAAC
WI-8172	136	C G G A C A	CCTTATTAAA ATTGTTTTCTT GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCTTAAAGTCATCTTCCAATCTCCAGGTACATGTTGGAAGATCACTGTTAAACACGAA ATCTAACCAATTAAACAAGCTTTTAAATCCTTCGGTAACCTCCCTTTTAAATGTTTCTTGACAT A/C/GJAGTACCTTTACAGGTATTACATTTCTCTTACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTACATGAAATAAACAATTTCTGTTGC/GJAGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCTTTATTGGGATTGCAAGCGTTTACAAGGTTAAAGACAAAACCCAGCATGGGATTTTGC CGGAAT ATTAGCGTTAAAGGAG/CJTTGAGTTGAGTCAACACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCAGGGAAGGTTAGTGGAG/GJAGAGATGGTCAGGCTTCTCTG TTCTTTAACAGCAGAGGCCCAACCTAGAACGCCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TOOCTGGGAG TTTAGTGTTCAC	GGGATTAGGAT TTTAGTGTTCAC	GGTGCCCTGGGAGACTATGGC/TAGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTCCCTTCTTATCCACCCAGTCTTCT
WI-8833	51 A T	TCTTCCATGGC ATATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTCTCCATGCCATTCTCTG/A/TJTGCCCTCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAAGTCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTtagccatgttggtAAAAGTTTCATTTTCAGTACATGGGTAAACCCAGGCCCTTCCC/A/GJT TATATCCAGGTATGCTACAAGTTCTTTAACTCTATCAGAAGTTATTATTACTGTTTCTTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCCTCATTTATTCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT/A/GJCTGCCCTGGCTGTTTGGCTCTGCCCTGCTGTTTTGGTTTCTT TCTCTTCTACTGGTCTTCTTTGCTTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGCATTG AGGATA	AGTCTTCTGA GCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA/C/TJATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCTGTGCGAAC/A/GJACAACATGCT TCGGACTTACCAAGGGAGATCGAGCTTTCCATATAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT	GGTAAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA/T/CJGGTCGAACAACAACATGCT TCGGACTTACCAAGGGAGATCGAGCTTTCCATATAA
WI-8895	32 A C	---	---	GTGCCACAACCTGGACACCAACCAACAGAAAT/A/CJCTCCGCTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAAATTATACCGGGATGCTCCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTGGATGTCACA/G/CJTTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCTGGCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTATATCTCAAGTAAGTACAGCTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA/A/GJTATATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAGAAATGGTAATG/A/JTTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAAGTACAGCTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATAGGCAGCTGTTAGAAAAAGTCT TGTTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC/A/GJTCCCTCTGCGGTTGTCACCCACATCCACAGAGCA GCCCTAGTGCAGGTGCAGCCACTGCCACCCACAGCCACAGGGAACAGGACCCCATGCTGC

WI-12108	40 C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
WI-5989	29 G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTTAAAAAAAAT CTTGTTAACTTGCCCTCCATCTTTCTTGCGTGAGGACACC
WI-12201	61 C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCTGGAGTGTATGTCCTCCAGCCCACTGATCACCTGCGATG[CT]GCCA GGTATGGTGGGGGTGATGGACGTGGGTTTGACGCCCTCCACTGCTCGATAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGCGGACGAGCTCTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCGCCACATACCA ACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCCTGCTG CATG	AGGGATCAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTGCTGCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT	TCCTTCTCTTT TGGTAGTGTG	AGCATGTAAGGAGCAGTTTATTTGATTGGTATATTCAGGTTTCTAACAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTTCTGTATACACATGGTGCTAGACATGGCTACACTTTA TACTTGTGCAATTAGTTGAGTATTGTTCTGCTCATAAATTTT[C]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCAATTTCAACAAAGTTAGCGTTTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T ---	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTTTCAGCATATGTATTAT[CT] TGAATAAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]AGGGCCCAACGGGAGGGTCCGGGAGACGACACTTTTCCCTGGG AAAG
WI-11321	67 A G T T T T	GGGAGGAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGTTGAAATCTTTTAAGCAGGGAGGAAAAATCCAAATAAATTTTTTAA A/GJAAGGTTTAGCTATTCCTCCCAATGCTATTTAATACAATTTGAGTTAGGAGGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G T G T G C C C C A	GGATAAATCA TGTGCCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCTTTTATGGATAAATCATGTGCCCCA[C/G]AGAGCCCCCAAGCTTGATGACAT TCTGTAAGGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTTGTCC



WI-11352a	69	T C G	AGCAGCAG ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAAGGAGAGAGATCATCTACATAAGCACAGCACATAGTGGAA AGTTCGCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCCCCTGA GCAC	TTAGCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTCGCTAGGCGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCCT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCCTGATGGTGGACACAGAAGACTTTCATATTTCTGTTTTTAAAGTGC TCTTCAGTTCAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAGAAATCAGC
WI-11388	88	C A A A G T T C	TGTTTGAAAT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGCCAGTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTT AAATTACACGTAACTAAGTTCATATAATTTAAGTTGGATACAAAGGCATTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGAACCTTA	GTACATTCAAG TGTTTTGTAA	TTCTATCATTCCTTAAATGGGAGGTTATGTGTTCTTGAACCTTAATAAATCTTGCTTTTACA AAACAGTGAATGATCTTCTTGTGCAAGGGAAGGGAACACTGAGTCTCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAAATAGATGGCAITTTGTCAGTTAAATTTGTTTTTGAATGGTGTGAATA TGAAATTAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCAACCAAC CAGC	TGOCAGGGCT TATTIG	CTGTCAGTCTTCCCACTAAACCGTGAGTTCAGTATGTCTGGCAGCACGCTGTCTTGTCTTGGTG TATTCOCATTACTGAATCCCAACCAACGAGC/AJCAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T T T A T T T G C A	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAGTC/TCTTCAGTCCAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTGTCATTTTATAACAATAAACTTTCTATTATCTATTATCTCTCAGACATACATTT CATGTATCCTG
WI-11384	35	A G	---	---	TTTTCTTTTGTGCTCTTTTGTAGTAGAAGC/AJGGAACAGTTGTCAATAGTACCTTCTGTGG TCCCTGTGTAGACAAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A C A G A C	GECAGCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATAGGCGGGCAGCCAGGAGCAGAC/AJGACCGGCTCTCAGTACACATT CCCCACCCCTGCTCGGTGCTCCCACTCAGGCTGGCATGGAGGGGCGAGCGTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTCC	ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCATAG/GGGAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGTTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTAGTTCATTACATG/AJGTACAAATCATTAGAGTCTTTACAAGTCAATAGAGTCTTTGGAT TTT

WI-14186a	52	C	T	A	GGTCATTTGAT GGAAAGACAC	AAGTAAACCA CCTGTAATTTT GTACC	AATGCTGGTTTATTGAGAGCTGTTGGTCATTTTGATGGAAGACACATA/C/TJGGTACAAAATT ACAGGTGGTTTAGTTTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A	G	GTGGGCTT	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAACCTTGAGCTTGCAAGAGAACACTTGTGGGGCTT/A/ GTTCAAACATGGACTGATAGGTCCACCCAGATTTCTAACTGGGTAGGTCGGGGTG
WI-12345	37	C	A	AAAGAGGAA	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA/C/AJ/CCTGAACCCCTCTGCAAGTATTCCT TTCCTGACCAGCTGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71	C	A	AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTATAG TTCAATGAATA ATTTCAA	GAAAGGCTGTAATTTTATTTTCAAATTTTGGAGTTTTTTCAGAAAAAAATAAAATGACAAGAACA CATA/C/AJAAATATTGAAATTTTCAATTGAACATAAACACTTAGCAGAGGAGGACITTTTGAT
WI-12310	46	G	A	AAAAGC	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTCCCT AAA	TTTGAAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT/G/AJTTTAGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAGTTTACAAATTTCCAGAAAGGCATTTTCTTTAAGCAG T
WI-12086	72	C	T	TTGGATTT	CCGGGAAAAAC TTGGATTT	GGAGTCTCCGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAAACTTG GATTT/C/TJCCAAGACCCGAAAGACTCCTCCAAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	TTTTATG	GGCATAAAGT TCATAATATTTC	GGAAAGTCTGT ACAAATCCCC	ATGTCTTACAGGTGTATTTTGTTAAGAGTTTGTCATCTAAATTTTTCATATTTATTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG/TJGGGGATTTGTACAGACTTTCTCTC
WI-11585	79	T	C	AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAGGAAAGAAATAAAACACCGGTAAATGGGAAAAATCAGTTCAGAGGTAGGAAGAGCTGGGTT TGCAAAAACAAAAT/CJGGAAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGAGCAGGGGTAGAGT TT
WI-11604	68	G	C	---	---	---	TTAGTTGGTTTCTCGAAACCTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGGACTTTTCCATGAAAAATAATTAAAGAGCTAAGGAATTCGACGCTCACCATTCTTC TTGTTACTCTGCAGTT
WI-11614c	108	C	A	---	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAAC/C/AJATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG/A/GJGG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	---	---	---	TTGATTTTACTAAGTCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAA/T/CJTACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTTTGCTAC AAGAACAATAATTGGCAATGA

WI-11626a	39 G A G	T C A C T G G A A C A T G A A G G T A	G T G G T A T G G C T A A T T T C T T A T T A T T A A G T	T T G A T T T A C T A A G G C T T C C A C T G G A A C A T G A A G G T A G [G/A] G A T A A G T G T A C A G G A T A A T A C T C A G A T A T T T A A A A T A A A T T A C T T A A T A A G A A A T T A G C C A T A C C A C A T T G T T C C A T T T G C T A C A A G A A C A A A T T G G C A A T G A
WI-11627	23 T C	C C T T C C T T C C C A T T G C C T C	C A T T T G C A A C C C A T C T C A A G	A C C C T T T C C T T C C A T T G T C C T C T T C J C T T G A G A T G G G T T G C A A T G G G A A G T A A A G C A A A A A G G G A G A T G A A A T A C T A T G A T G C C T T T T G T G G C T A C T T C C A T T C G C A T G T C A A G T C C A T C C A T G
WI-11636	61 A G T C C T	G G A C T T A A A A A G A T C T G C T T A	A G A A C T T G C T A A A T A T T T A T G T A A C A C T	T C A G A A A T G T T G C A A G A A A T A C T A T T T G T A A G G T G G A C T T A A A A A G A T C T G C T T A T C C T T A G J T A T A T C C A C A T A A C T A G T A G T T A C A T A A A A T A T T A G C A A G T T C T G T G A C A G G T G C T C A G T A A A C A C T T T G A C T C C T T T T T G G T A
WI-11637	119 C G T	A T T G C T C A T C T T A C T C T G A C C A	G A C C C A G C A A A A A G A A T G A T T	G T A C C A T T C T T A T G T G G C A A A T A A G C A A C T G T G A G T A A A C G A G G C A G C T G A A T A A A T T T A C A G T A T A C A A T A T T A G A G A A T A T T A T G T T G C A A T T G C T C A T C T A C T C T G A C C A T C J G J A T A A T C A T T C T T T T T G C T G G G T C C A G G A C C
WI-11654	37 G C C T G	G C C A A A A G A C T A T T C A G C A A	G G C T C T C C A G G A C A G T T	A G T A G A A C A T C A G T G C C A A A A G A C T A T T C A G C A A C T G [G/C] A A A C T G T C C T G G G A G A G C C A C T C C A G A G C T A T T C T A A G A C T T T C T G T G G T T T C A T A C T C T A C T C A G A G T T C A C A C T C A T A T T T C A T A T T T T T A T T T T G G G T G T T G G G T
WI-11656	28 G A A A	A A G G A A C T G C A A A	C A A G G C T T T G T C C T C A A G T A A A	A C C T G A T T G A T T T A G A A G G A A C T G C A A [G/A] C T T T A C T T G A G G A C A A A G C C T T G C C T G C A G T T G T T T A A A T G T C C T G A A C A A T C A G A T T C C C A G C C T G G A T
WI-11680	55 T C --		---	A C A G A T A C T T T C C A C G C A A C A T T T C T G A A A T G A A A G C T T T G A T T C T C C C C T T T T C J T T G C A T A A A G G C T G G A A G G T G T T G C C A G A C C G T A C A T C T T T T
WI-11696	47 T C A G G G A C A G	T T A T C A C A G C A G G G G A C A G	G G C A T T A G A G A A G C C A A C C T T	G T C C A A G A C A A A G A T A C T T T G A C A T C T T A T C A C A G C A G G G A C A G T C J A A G G T T G C C T T C T C T A A T G C C C A C C A T C T T G T T T C A G A A T C T T C C A C T T C G C C
WI-11702	69 C T C A G C A G	G A A T A A T A C T G A A A T A A C C A	A G A C A A C T T A A G C A A A T T A T A C T G A A A	T T A C A T G T G T C A A T G G T G A C A T A C T T T C A A T A A T T A A A A A T C G A A T A A T A C T G A A A T A A C C A C A G C A G C J T T T C A G T A T A A T T G C T T A A G T T G T C T A G A A A A C A C T G C T A A T T T T T G T T C T G C A G A
WI-11706	60 C T T C T C T T	T G G C T G G A A T T T T C T C T T C T T	A T C A C C A A A G A A C A A A T T C C A	T G C T G A T T C A T C G C T T C T A C C A T C T G G C T G G A A T T T C T C T T C T T G T A C A A T T A T T G C J T G G C T G G A A T T T G T C T T T G G T G A T T T G C C C C T T G C T G C T
WI-11709	105 T A T T C A G T T T G C	A G A A G C T T G C T T C A G T T T G C	T C A T T T C T C T A A T T T A C G G G A	A A T A T C A T C A C T C A T A T C A G G C A T G T T A T A A A A A T G A G A G A T A T G T C C T T T T T G G C A T A C T T C A T C T T C T T C A G G A C A C A G A G A A G C T T G C T T C A G T T T G C J T A [G] T C C C G T A A A A T T A G A A G A A A T G A A T G G C C A G A T G G A T G G A A A
WI-11710	103 C A C A G T C T T C A	G C A C C T A G C C T C A G T C T T C A	G T G T G G A G A G G G A G G A G	T T A T A C C A T C A A C C T G T C C C A G C T T T C C A G C A C A A G C C A C A C C A C A C T C T A G A C A C G C C T T C A C T C C A G T C C A T T C T G G C A C C T A G C C T A G C T C A G T C T T C A C J A C T C C C C T C C T C C A C A C A C T C C T C

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCCCATCCTG TGCT	AGAATGGAGCTGTGGGGAGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGGACTGGGAAGA
WI-11715a	49 A C A A A	GCACACAATG TAAACACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGGAGGACATGCACACAATGTAAACAGACAAAA/CJTGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGGACTGGGAAGA
WI-11727	43 G C T C A C A	AACATCCTT AAAACAACATA	OCTGTGGTTG TGTTGCAG	CTGGATTTCCTATACCTAACAAATCCTTAAACAACTATCAACA/GCCTGCAACAAAAACACAGGC AAATGAAAAACAGATGCCACAGACAGCACCACCCACACATGGCACACAC
WI-11728	16 C G ---	ATCTGTGGTT TCGCCCTG	---	TTTTATTATCAAACTC/GCAATTCCATTTACAAAATGTAAATATCATCAGCTCCCCATCCACTTT CTCCATCTTCTATCTTTCCCAACCCTACACTTTCTCCCTACAAACCCGGTTCCAAA
WI-11758	61 A G T C C C T G	GCCTCACAAA GTATTTCTAA GAATATAA	TGATGGCCCT GTGTCTA	TTTTCCCTTTTATTAAAGTCCGTATACTAACTAGAGGAGAACTGTGGTTTCGCCCTG/GJTAG ACCACAGGGCCCAATCACACAGCTTCTGTAGAGACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G A A T A T A A	GGCTCAGAGA GCAAGGGAA	AAAGTGCTCA TCTGTGAACTC T	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT/GJTAGATTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	GGCTCAGAGA GCAAGGGAA	---	AGCAGATGATATCTGCCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAGAATT ATTATTGCCCTCTTTTTCCTCCCTC/GJGTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G C A A C C T C T G	GCCTCAGAGA GCAAGGGAA	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAAACCTCTTTATTAAATGGGCTCAGAGCAAGGGA/C/GJACACAAAAATTTACAGTCTGA GTTTTGGCGCAGAGACCCCTCTCCACCTTTTCATGCCCTGTGTGTACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G A A C C T C T G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAAACTCTGT/GJGTAGCCTGCCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACITTT ATAAAAA	TTTTAATTCCTCAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/AJAGT GATTTCTCTCTTCTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T A A G T T A A A	GTATTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTACTAATTTCCATTTCTCCCTCTTTTATAGTTTTAATGTGTGTTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA/C/JTGTGACAGCAGATCTTCAAAGTTTGCTATAGACAATCTGA AAATGGGTCTGAAC
WI-11906	52 A G A T C T G A A	TGTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTATAACATCAAAAGAAATCTGAAT/GJTGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATCTCAGAATGCCAGAGTAGATGAACCCCTTTACAG

WI-11909	78 A	TTGTGTTGGG TGGTCAAG	CTCTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGGTCAAG/GTGCTATTTCAGAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGCAAGATC
WI-11806	60 T	CATGAAGAGT GGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCAATTTAGCATCAATTTGCCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTTCAT/GJGTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31 CA	---	---	CCCTAGTGAATACAAACCTTTGTCTGGAGAC/GCAGCTAGTCTAAGAAACCTTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGAA
WI-11965	65 T	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATCACAAAGTACAACTGCTTATTTTCTTGCTTGAAGATCAGATCTCTGGTTTATTAAAT/ GATCAACATTTCCACACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTGAAACTGCAGAAAGGGCAGGACAAAACAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAATTA/AAATAAATACTGTAAACATTTCTCTCATTTCTCTACGA ATACITCTTTTGTATTTGCAAAATCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 CT	---	---	TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGACCTTT GTGTTTATTTCTGTTTCAACTAAGGAC/CTAGACTTCAGAAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCCAA
WI-15488	69 CT	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC/CTGTTACAGAAATGAAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49 A	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTGAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTAA/GJGTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAAACCTTTTCCCAATTTACAGACAAAACCCAGT
WI-11070b	135 CT	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA C/CTGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110 GTT	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATTTACCTCTAGCGCGGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCAATTTCTCTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142	G A ---	---	CATGGTTCGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT
WI-11076a	106	T C AGGA	TCCTGCTCTGG GTATGTGAC	G CATGGTTCGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT
WI-14263	49	T C GGCATATTC A	GACA	G ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAAT/CJTGTCCCATACTAAT TTTGAATAACCTAACTCTCCCTTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGAGCAT/CJTGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTAAAGGAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28	T C ---	---	G GATTTGTTTTATTCAATCTCGCTTTTTCATTTTGGCTTTTAAATAGAACAG/GA/CJTTTGATTTTTAGTA TATGACATCATCATCATGAATTTTTTCTCTTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50	G A TAGAAC	ATCAAAG	ACCTCTTTCTGATGACACTTGACCTGTACCTGTAAAGGGTCTAGAGAGAAAAAGTAGTAGACTCTCTACTTGGC TACAAATCAGGATGCAGGGCATGAGAGGATTCCCTCTC/CJGTCCAAGGGAAGGCTTTTGGC AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTCTTTGTTAATCTGGAGCAG/CJATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG
WI-13951b	88	G C ---	---	G AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAAA/CJTJAGACCCAGATCAGAGGAAGAG ATGGCTTTCTTTGTTAATTTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG
WI-13951a	39	C T CAAAA	TTCTCTGATC TGGGTCT	G GAGACCAAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCTGACTGACCCCCAGTGTTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGATCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTTGTCATGGC
WI-13264	25	G A TTGCCAT	GGAGGGAGAG ACGGGAATA	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA/CJGATGCAAAATTTGTCCTTTCATGCA TTTGTGGAGCAAAAGTACTAATCTTGCTCACTGTCATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAC
WI-13960	39	A C TGATAGA	C	AACTCTTTATTGTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAGCCTTCAG/CJTJAG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTGCCACCAAGGAACCCAGGCTTGGCT
WI-15843	62	C T CAG	CTCTGGCTCAG ACTTGCTCT	

WI-13983	52 G A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTCGGAACATAGAAATCTCTCTCCACTCTCTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGATATGCACCTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAGGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCTTGAT[G/C]TTTCTCTTGGCAACTATTTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAGAAAGGCCCGGAAATATGAGTGAGACTCA
WI-14284	55 C T ---		---	ATTTCAACAAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCTTGA
WI-14288	85 G C	CCGCTGCTATT CCACAGAT	GGTCTCTTCC ACCAATCTT	ATGACCAGACCAGAGCCCTGTCTTATATGAAGACAACAGGTGGCCATCTTGGTGGAGGGATA CCGCTGCTATTCCAGAT[G/C]AAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T	TGATGTAGTTA CCCCACTAAT	CATAATATTGG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCCTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGGAATTTTTCAGAGAGAATAATA
WI-13529	42 T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCATTCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCTCGAGGGTTTATAGTCTACAGGGGGAACAACCTCTC A
WI-13859	84 G A ---	TTACCA	GCTT	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAATTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29 T C ---		---	TGAAAGGATACAGAAAAAATCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52 G A ---		---	TTTTATTGTTTGGTAGAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACCGCGGCCCTTGAATCTGACATTCACAGTCAAC CGTAATAGAAAACAGAGCT
WI-13477b	61 A G ---		---	TTGGTTTTTAATACCTCTGTGGATAAAAGGACATTTTTCATTAGCTTGTCTTCAA[A/G]GAC AGAGAAATAAGATAAATACCTTAAAGAAAATTAATAGAAAATTAAGGAACATGTACCAAGGTGG TTTAGACTCTCTCTCAGTT
WI-13477a	32 A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTGTGGATAAAAGG[A/G]CATTGTTTTTCATTAGCTTGTCTCAAAGAC AGAGAAATAAGATAAATACCTTAAAGAAAATTAATAGAAAATTAAGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT



WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCATGCAATGCAATTTATTTCTGGCAATAAATTATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAGAT/AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G A A A	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAATAATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTT/GJACCAAAAAAATTAAGATTTTTTGGGACAAATTCACATGTT AAAAAT
WI-13582	43 C A A G A C T G G G G A	TGCAATCTAG AAGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA/CATJTGAAATCTAATCTAAGCTGCGCAGAG AAATCAAGACCGATGGTGAAATCTGGGCGAGCTTCAAAATTTCTGCCTCTCTAAAAACATTTTCAC CCAAATTTTCATTATGGC
WI-13857	28 A G		---	TCTGAGTTGATAAAATGCTTTTCTGAAC/AGTACATTTTAGGTATCTGGCACAATTAACCAAAATGT CTGCCATTTTGTGTAGCTTTCATACAGTACAGATTTTCATTGATGTGCTGCCACATCTG
WI-15809	77 T G T G A A A T G C C	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAA	GTTTTAAGTTCAGAGATGTGAATGGTTTACAATCTGAAGCTGAAGTTCAATCTTTGGTTTTCTGTT GTAAATGCC/TGTTTACAACATTTGAATAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T		---	TAAATCAGTCTGTGTCAGAAAGAACAGGACTTGATCAAGCTTCCAGCCCTCACACTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAAAACCAAGAGAAGAA/ATJGGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G A A	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTTA GCTGCAGTAATAC/TGJGCAATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAAGT GCTGAATGCTCTCTC
WI-15801a	24 G A A T G G G A A G C	TTTATCCAAAG AATGGGAAGC	TCATTCAGCC AATGAAATG	TCITTTATCCAAAGATGGGAAGC/GA/CATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAAGT GCTGAATGCTCTCTC
WI-13763	59 T C G C A G T G A T	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT/CJAGGG GCAGGTGTGGGGCAGGGTGGGGCTCTGAGCCGAGGACAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A A C C	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACC/T/JAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCCCAACATTTGATATTTTCCGAGGGCAAAAAGA GAGTCTTCCAGAAACTC
WI-13789	62 G A A G G G A G	TTGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAGGAAAAAGAAAGAAACCATCAGTGAGAAAACTCAAGAAITGGATGGCTGAGGGAG/GA GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCCTCTCTT GAGGTCCCT
WI-13594	66 G A A G C	TTTTTAACACA GATCACAAAA	CCTTTCGCGCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCAAAAAAGC GATTCACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAITAGGCCAAACAGCTGC



WI-15625	40 C T ---			GTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[CTGTGTCCTCACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCAACCAG	TCCCCACCCCA OCCCT	GTCTCACTTCTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAAGAA[CTGJAGGGGTGGGTGGGAATACTTAATCAATATTTGTGGAAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC T AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACITTAATGAGCCAGCATCCAT[GTJCCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAAACAAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCTCT TGATTCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAAATATTTA ATATTAAT	GATAGGAAAAGAAAGATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[GTJAAATCTATTAAATTAATATTGTCATGAGGTATGCACCT GOCA
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACTTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTAC TTTTAAAC[ATJAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[CTJACATGCAACAATATAGATGATTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAA	CAATACATT GCATTTTCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTATCAATACATATTTGCATTTTCTTAAAA AAAGAAGACATTT[AGJTTTACAGAGAAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAAATTT
WI-13909c	93 A T ---		---	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCTTCTCACACT CTCTTCAAACCTG[GAATAATCTTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCTTCTCACACT CTCTTCAAACCTG[GAATAATCTTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---		---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATTTCTGGAC[CTJATGGGAACCTTGAAAAAGGCATGGCAGTGAGACCAGTA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATTTCTGGAC[CTJCTGGACCATGGGAACCTTGAAAAAGGCATGGCAGTGAGACCAGTA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAAATTGACAAATCACTAGCTGCTTTTGTGCTTTTGGAGACTACCATTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[GTJAAAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGCTTCCA AA	AAAAATTGACAAAATCAACTAGCTTGCTTTTGTGTCG/AJTTTGGGAAGACTACCAATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAGTGTGGAAATCACTCATCTGTGCG TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGTCATAAAGATATAAAATTTGCTTCAT TTTAAACTAAATTTAGTGTGTTTT/CJTAAATATATGAACCTTTTGGTGAATTATGAACGTGTACCAAAG C
WI-15747	88 T C AGTGTTT	TGCTTCATTTT AAACTAAATTT	CATAATTCACG AAAAGTTCATA TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGACACG/CJTGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752b	117 CT ---		---	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGACACGCGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752a	106 T C AGTCTGGA	CCCTTCGTGTA AGTCTGGA	COCTCCGTAA AGGTCTCC	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGACACGCGACACCTTTTACG GAGGGATTCCGGACAAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACACCTTCACTGGGTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGATACATGATTACTT/GJGGTTTCCAGAAATCTGGATAC
WI-13744	115 CT AAACTGAA	TGGTGTGAAC AAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACAGTAATGGAACTTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGCTGAACAAACTGAAC/CJTGCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 CT ---		---	CCCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGAGCCCCCGTACATACCTTAT CJTAACCATTTTCATCCACCATTGTGAAAATCTCATCTCTCTGGGTCTGGATCTCAAAAACAGAT CJTAACCATTTTCATCCACCATTGTGAAAATCTCATCTCTCTGGGTCTGGATCTCAAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGATAGTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACCACACTGAATATACTGAATTAACCTTTCAACCTTTTCATCCATTGAG CJTAACCATTTTCATCCACCATTGTGAAAATCTCATCTCTCTGGGTCTGGATCTCAAAAACAGAT
WI-13810	106 T C AACTT	GTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCACACATACATAGATCAACAGAGAGTACCACAGTATGCTTTATTTTGCA GGTATTAATGGTCTCTAAATCGATACATCCAAAACCTTT/CJAGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 GT CACA	ATTTTATTGAC ATTAAACTTG	GTCTTTTGATA TGCTGCTTAGT TTT	GGATTTTATTACATTAACCTTGACACAGTTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAAAGAACATATACATAGAGATTGAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/GATTAGTGACACATAGCTGTACACACACAGTG
WI-13785d	72 GA ---		---	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC/CJCAAATG AACAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC/CJCAAATG
WI-13785c	56 A C ---		---	AACAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC/CJCAAATG AACAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC/CJCAAATG

WI-13785b	40 C G ---	---	---	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13785a	27 T C TGCTT	TGTTGTGACAG CTATGTGTCAG T	---	TCAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13793	88 C G ATAGG	GGCAGGAGGA TTTGTACT	---	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTACCCCATTTGATACACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAATCTATGACTTG
WI-13794	52 A G TTCTTCTC	AGAATGGGCTC TTAACCTTGTA	---	TAGTCTCTACAAATCCTTCAATCCATTTCTCTCTCACCCCTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCATTTCTTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTGAACCAT TCTAAAGTGCC	---	TCATTTAAGTGCACITTTGAACCATGTGTAGACTGC[C/G]GGCACITTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTTGAATTCCTCAAGGAGGTAGTCCCTGTTTCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	68 G A C	TTTCTCTCCC AGGGTCTA	---	GTCTTTGCACAAAGTCTCCCACTGGTTTGAGTTTCCCTTCTGAGGTTTTACCCCTATTCTTC[C/G]A TAGACCTGGGGAGAAAACACATGTGTAGTGGTCTCAGGACATGAGCAGGCCGTTTCAACAAGAT GCTGGCTAAGGGCTTC
WI-14065	29 T C AATT	CAAGCTGAATC TGGGATCTC	---	AACTGTCTTATAAAGGTGACAGGCAATTT[C/J]GAGATCCAGATTCAGCTTGTCTCATATAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGCTGCTTTTAACTCTGAACATTTTGAAGCAGCAA
WI-13446	22 G C TCACTCATCA	AAGGGAATCA AAATCAGAAG G	---	TGCCATGTTCTTCACTCATCA[C/G]CCTTCTGATTTGATCCCTTCTGCTCTGTAAATTTTCTTC TTCCCTTTTAGGGCTAGTCTGTTTAGAAATCTGGTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGCCCTAATT
WI-13725	56 A C TGGGTGC	CCTGCTGTCTC GGGC	---	TCACACAAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTACAAAACTTGACCAGGCAGTTAGAAAGCAAGGCATGGTTTCAGGATG
WI-15702d	107 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAATCTAAAT[C/J]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAATCTAAATCTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAATCTAATGGGTTCTTTGAACAAATAGTTT TGA

5

WI-15702a	48 G C A A A G	A A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A G [G/C] G G G T A A A G G G G T G A G G A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A A C A T A C T A A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T C C A C T G T A T C C T C G G G T A A G T T T C C T C T C T G T A G A [G/C] G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---		---	T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C G G G T A A G T T T T C C T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13808	62 G A ---		---	T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A T C A G A G A G G C C A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T T C A G C A A C A A A T C G A G G T G C A A C A G G G T T A T T T C A C A T T A A T A T A T T A A C T G G A T T T T T T G T C A A A T A A T A G G A [A/G] T T C T C T T T A A T A A C C A T C T C C T C A C T T C A T G G C C A G T ---
WI-14373	95 A G ---		---	A G G C T G T T T T T G A G G C C T G A G G A C C C C A C A C A T G A C A C G T A A G A C T G T A A C C A T G G T G A T T A T G A C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A G T A A T T A G G A A G A G C A A G [C/T] G C A G T A A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C A G A C T T G A G A G C T T A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T A A G G T T A A G G T T A C A A G G C C A A
WI-14085	31 A G A A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T A	T G C A T T T A T T T C A T G T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T T C T A A A T T T C A C C T T A T T G T A A G T T A A A T A A A A C T C C T A T T T C T T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G A G A A T G A A G G A G G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A G A A A T C C T C A T C T G G G G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAA GGGTTATGCA CACC	ATCATCTGTT TGAGGTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTGCTGCTACTAATATCAATCCTAGTAGTATTTCTTT TACTTGTGCTATTAAACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAA[A/C]ACCCACCATTAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGTATTTAA[A/A]GJACAAGCGTCTGCTGCTGCTGAGGGCTGGGACCACTGC AGTGGGGCTCCGGCAGCTGCTCTCTCCAGGACTCTTCCACCAACCCC
WI-15937	24 A G A	AACTGAAAC GTATTCCTCC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCTCTCCA[A/C]ACACCGTAGAACTTTAAAGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAGGAGTTTCAGGTGATACAAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A			ATGTTTATGATCAATTCOAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAGCTCAGTCACTAC
WI-14124	92 A G			GACAAAGAGGAGCTTCTGTAGTCCAGCAGGCGCAGAGGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCAGGACTA[C/T]GTGGCCATGCCATTCCTGTAGTGAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GGCAC	GTTTATTTCTCACAGTCTCGAGGTTAGAACTGTAGATGAGGATATCACAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTCTTCACAT[G/A]GCCCAAGAGAGC AGAACAAGCTCTCTGGT
WI-14136	120 G A	GCTTCTCACC ATGCTCTCACA	CTTGTTCTGTC TCTTGGGC	TTGTTGTTGGCACCAGAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23 C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTATTCTATAATTTCAAACTTGGAAAGCAACCAAGATGCTCTCAGTAGTAGTATTTCA GACAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	TCCTCAGTAG TAGTATTTCA GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATAIT	TTTTTAAAGAGTGCCTTCACATCATTTATATTGATTGACACAAAACCTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOOC
WI-15953b	59 C T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG	TTTTTAAAGAGTGCCTTCACATCATTT[G]TATATTGATTGACACAAAACCTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOOC
WI-15953a	26 T G A T		A	

WI-14631	82	G A ---					TGAATTCATGGACAGTTTTGCCCTCTGTTTAGTGAAACCCCTACAAGCACTCTGCATAGTCCGCTTTCTGTCTCTTTAAQ[G/A]TGCCCTGGTTCCCTCTGCCCAAACCTTTAGGATTTGGGCCTCCTCAGGGCCTTGCTCGA
WI-8053	24	A G ---					ATCACCACCGTGTCTAAGAACAAC[A/G]TCTTCATGTCCAATCATATCCCCGGGACITTTGTCAACTGCAGTACACTTCTGCTGATTGAACCTGGCTTCTGAGGGAAGCCTCCTAGAGGCCAGGTAAAGGGGTGCAGCAGTGAGGGGTATACTGGCTGGCCAGTTGGAAACCACGGAG
WI-15964	99	T A CTGGAGGTA					CAGAAACCTCTTCTGTGTATTAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTA[T/A]GCAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G A GGCAC					CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGGGGAGGAGCCT
WI-12179	96	G A TGGAGGTCA					TAATTTAAAAACACGCCCTTCCACATAGTGCAGGCTGCACATTTTCTAGAAGGACATGAATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGAGGAACAG
WI-14651	49	C G ATTGT					CACAAATAGTGAAATATCTGAGCAAGAATCATCTCATTTAAAAATTG[C/G]AAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---					AATGTGGACTTCAACAACAGGGTTTAAAGCTAATCTAATACTTCTACAACATTCACACATTCAGAGCATATAACAAGAATATTACAGGCAGCTAATGTATTAAAT[T/A]AACCATGAAAAGAAAAAACTTG
WI-13473	31	CT ---					ATCTAGATGTCAGCAAAATGGGCTGAGACTG[C/T]TGCTGGTAGATGCAGTGTTTGTATGTTTCTACCTATTACAAAAATTACAGAAATATGGCTTGGCTTGTGCAAAATGTTTATATCACAGTC
WI-13967	103	A C AAATAAAAA					AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAGATAAAATATGTCAATTCAGCAGTCATTTAAAAATAAAGACTACAGATACAAGGAATAAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A G					TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAAGTAACAAATGAGTTTACACAATTAATAATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C G ---					TTTTGTGTTAAGAACACAGCATTTTGAAAATAAACCTATCTGCCCATG[C/G]TTACAGCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T CGTCT					TTAGAAAACCTGATAAAGCAACACAACTTTTGGGAAAGCACCATGGCAGCTCCTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---					ACATGGCAGATACAGAGCTG[C/G]ATCTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTCTCTGACCGTCTGGGAGCGTTGAAGGGGTGACCAGCACATTTGCACATGCAAAA

WI-16002	59	T C A G A T T T C	G A T A A C A T A A A A T G A T C A T G	G C C A T C T C C T C T T T G A C T T T T	C C A A C A T T T T A A A C C T A T G A C T G G T C A T T G A T A A C A T A A A A T G A T C A T G A G A A T T T C A T T C J G T T A A A G T C A A G A G G A G A T G G C T A A T G A T G C T G G G C T
WI-15361b	101	A G A	C C C A C T T G A A C T C A A G T C A T C	C T T T G T G C T A A A A	G T G G A A T T T T A T A A G C C A T C A A A A T T C C T T C A C A C T A A T A C T G T T G A C A C A A G A T A A C A C A T C T T C T T G C T A C C C A C T T G A A C T A A G T C A T C A J A G J T T T A G G C A C A A A G G T T T T A G T T T T C T C G G G A A T C A A G T T T A A C C A
WI-14759	73	T C G T G C G G	G C G T T T G A C T T	T C C C A C A C T G C C C C C	T G A G T T A C A A C A A T G A G C A C A A G T T A G A A A A T T G G T T T T A T T C A A A C T T C C T A G C G T T T G A C T T G T G C G G T J C J G T A C T C A A A T G G G G G C A G T G T G G A C G G G A G G A T T G C A A C C A G A G T T C A T A C T G C A A
WI-12535	50	A T T A T	C T A G G A G G T T G A G G T G T A G A	G C T C A C G A G A A G A G A G G A A	T C C T A A C A T T A T T C A G G T G G T A C T A G G A G G T T G A G G T G T A G A T A T J A T J C T T C C T C T C T C T C G T G G A C C T T A C T G A A G A C A G A T G C C G T T C T T G T T T A T C A G C T G A A A G G C A G T C T C G C C A T C T T A A G A C C T G C C C T C C
WI-13805a	112	G A G G G A A	A A G G C A C A C	C T C A G C C T G C C T T G A C C	T T C A T T C A T T A T G C T T G G C T T A C C A A T T T T T A T A G C T A T T G G G A G G C A G A A A G G A A T T T T G G C C C C A A A C C A T G A G A T T G G T C A G A A A A A G G C A C A C G G G A A J A J G G T C A A G G C A G G C T G A G A G T C A C A T T T C A G A C C T C
WI-12340	18	T C ---		---	A C A C A A T A A T T C C A T T J C J G A G T G A T T A A A A C C T A T T G T T G T T A G A A C C A A A A A A A C T A C A A G A A A C A T T T C A A A A C C T T T T T T T C A G G C T G A
WI-14808	52	T A C T A C C C T G T	A C C C A C C A C A C T A C C C T G T	A T G T T A A G A T T T T	C T T T G A A C A C T T T A A G C A A C A G T T A A A A A G T A C C C A C C A C A C T A C C C T G T T A J A A A A T C T T A A C A T T G T G A T G C C T C T G C A T C A A T T T T A G A A A A C A A A G A A A C A C A A C T G A A G C C C C A T G A
WI-14816	29	A T ---		---	A G T T A A A A A A A A T C G A G T C A G C A T T T A T J A J A A A A A C T G G A C A C G C T T C T A T A T T G C A A G C T C A T T C A A A T G C A T T A T T T T G T A T C C C A A G C C C C T G A A A C A C A T G A A A A A A T A T T A C T A A A G G A A T G T T G A T A C C A G C T A C G A C T T T C
WI-12542c	71	G T ---		---	C C G T G T T T C A T T G A A G G C T A T T A G G C A A A C T G A A C A C A T T T A A T G T C A T C C A T G T G A G G G C T C T A G A T C A T G J G T T A G G T G A T T G A T A C A A A T A C G A T C C A T A A
WI-12542b	70	G T ---		---	C C G T G T T C A T T G A A G G C T A T T A G G C A A A C T G A A C A C A T T T A A A T G T C A T C C A T G T G A G G G C T C T A G A T C A T J G J T A G G T G A T T G A T A C A A A T A C G A T C C A T A A
WI-12542a	45	C T T T T A A A	G C T A T T A G G C A A A C T G A A C A	T C T A G A G C C C T C A C A T G G A T	C C G T G T T C A T T G A A G G C T A T T A G G C A A A C T G A A C A T T T A A A T G J C J T A T C C A T G T G A G G G C T C T A G A T C A T G G T A G G T A T T G A T A C A A A T A C G A T C C A T A A
WI-12173	57	C T C A A A A A	G G A T A C A G C A G T A A A G A A T A	C C A C C T C T A G A A T G T A T G C T C T	C A C C T A A A T C A T T C T A G A A A C T G G G G A T A C A G C A G T A A A G A A T A C A A A A A A A A T C C T G C J C J T T A T A G A G C A T A C A T T C T A G A G G T G G G A A G A G G C A A T A A A T A



WI-14836	28 T C ---			---	TC TTGGAGGATAGAGGACAGAGTGTTC/GTTGATTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTGTTTTTGCTAATTTGGCCACCCCTATAAAAAGCAGTGCACCCAGAGGCAG
		TGGTGACAG	TTTGTTTGCTA	TTTGTTTGCTA	ACATTTCCCTTATGATAGCAACAATAATATGATGGTGGTGACACGGAAATACCTTAATATTTAA AGTTTGTAAAAGTAGCAACAAAATTTGAGTATATACTATAAGTGATAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14856	60 A T A A			---	ATGGCAATTTACTTTTATAGCAATGAACAAATATTTGTCAAAGGGCAATATTTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCCTATTATTGATTGCCACT ACCTGGC
WI-14863	61 G A ---			---	TTTTAATTAACGTAAAAAGGAGGACATTCCAAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGGCCCA TTGCTTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14867	46 T C A	GACATCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TGGGGCTGCAG ACACTC	ACGGAGTCGCTCTGATGTATCTGTCAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAATT AGAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAATGGCCTGACCTCATCAAAAACATCA ATGTCATGAAAAACACAAA
WI-14733	98 G A A			---	TTTTGTACCTATTCCTGTTTCAGTGTCATGTACAGGAAGATTGTCTCATAGGTTGCCACTAAGGAAA ACTTCTCCAT[C/A]AAGCTGCCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGCTGCATCT GCCTGTGTTCTGCTT
WI-14898b	79 A C ---			---	TTTTGTACCTATTCCTGTTTCAGTGTCATGTACAGGAAGATTGTCTCAT[C/A]AGGTGCCACTAAGG AAAACCTTCTCCATAAGCTGCCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGCTGCATC TGCTGTGTTCTGCTT
WI-14898a	50 A C A	CATGTACAGG AAGAGTTGCTT	AAGTTTCCCT AGTGGACCT	AAGTTTCCCT AGTGGACCT	TGGTATTATTTCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCCATCAATCAGTACTCCTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14907	48 G A GGACTCTGAC	GGCACACATT CCAATACATT	TCTGCTGCAAG GGGAAT	TCTGCTGCAAG GGGAAT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCCCTGGT[C/G/A]AAGGTCTTTTC CTGGTTTGCAGACAGATACCTTGTGTATCCTCACATGGCAGAGAAAGAGAGGAAATATCT
WI-14911	52 G A C	CAGTTCTGGT	CAAACCAGGA AAAGGACCTT	CAAACCAGGA AAAGGACCTT	CTGATGCTTTGACATCTGGGGCATTTGCTGTCTAGAGAGACTACTTCTCCTGGGACCGCAATTC TAGTGATAGTAGGACTCA[C/A]CCTGCACGTGCACCTTTTATATACAGATCAACCAATCCAAAAC CTACACCTCCAACACCT
WI-14913	88 C A ---			---	ATTTCTTGATTGGCTGTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/
WI-14914	66 G C A	CTGGACACAG TTTCTCTAGC	CAAGCCAGGA CAATAAATTC	CAAGCCAGGA CAATAAATTC	CJGAATTTATTGCTCTGGGCTTGATGGCTTTCACAG
WI-14926	49 T C ---			---	GTTTATTTCAAATGACACATCCAGATTGAAATGGGCACTTAGCGAAT[C]ACTTGTGGACCACA AGACTTGCTGAGAACATGTTCAAAGACAGTTTCAAAATAAAAATTTTCTTAATCAGGTCCA



WI-16083	89	CT	AAGGAT	ATGTTTAAACA CAAACATATC	TGGAAGAAGATT CCAGCC	GCATCTTTATTACCACAGAAACTCATTATGTCTTAAATCAATGTTTAAATATAAAGCATGTT TAACACAAACATATCAAGGATC/TJGGGCTGGAATCTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55	CT	CTCATGGAT	GGAGGAGTCC	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCTTTTCCACAGGAGGAGTCCCTCATGGATC/TJGCGGTATTG GTTGGTTGGTGATTGGGGAGCACAGGGAGAGCAA
WI-14946	47	TC	---	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTGGCCCCAGACATAACA/TJCTCTAAATCATCTCTCTA GATCAGGGAGTCATAAGGACCAATTAGGCTCATTACACACAGTACTTTATGGAAGGATT
WI-15987b	80	AG	---	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCCTCCACTATGTGAGGACAC TAAGAAGATGGTCA/TJCTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-15987a	32	CT	AG	CACAAATTA GGGTCCCA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGTCCCAAC/TJGAGGTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGTGATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-14948	56	TC	G	AGGAAACTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTCTTATTGCCGTTCTTCCAGGGAACAGGAACTGCTAACTTGTGAGT/CJTCCAACA ACTGATGAAGATCATCTTCTGACCATAGCGAACCTGTGAAGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	AG	TTGA	CAAAAGCTA TTTCTACAC	ACAGGAATGTC AGAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC/TJGTAATATACTG TTTTCTGACATTCCTGTTATCAACTCTCTGAAAAATC
WI-14958	83	AG	CAAGG	AATAATTAT CTCTTCTTT	AATGCATTGAT TTGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTATTCAACTCTAAAAATCCAGATGAAAAATAATTATCT CTTTCTTTCAAGGG/TJGAAAAACCAATGAATGATTTTTCAGTTTCTCCAGGCTTTGAAGCTGC AGCAGAAAAATCAAGGA
WI-14978	35	CT	TCGTTCAAAG	GTTGATTGCT TCAGTGGTGT	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTGAATTTGCTTCAAAG/TJGCTTAGAATGGAAGATTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	GT	T	TATTGGATTTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTGAGTGGTATTATTGGATTTT/TJTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	CT	GAAGCTGCAG	TGCATTAAAT	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTTAAATCATGCTACCAGCCCATCTAAGCCAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG/TJAGGAAAGCTGAGACATAGCACCCCACTGATCGGAAAAAGAAACGTA
WI-15002	72	TA	---	---	---	AAATCTCTTCTTCCACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAAATGCTCTTGA TTTCCT/TJTTGAGTTAGGCTCAATGGGCTCTCCTCAAGGCTGACCTCAAAAGGCCACGTT
WI-15000	90	GA	GTCTAA	GACAGAAAA GACTCAGACT	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA/TJGTAAGTTTGTGAGAACTAGAAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCT CATGTACCTAT GAAATAA	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTTTATACACAATACCTTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTCAAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTACAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAACA/AJTCAAAAAACACTGGGACATGCCCTTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC A	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCCTCTGAAGACTCCATGCAGT CAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGOCCTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/T/AJCTCAACAATACCATATACAACATACT TTCAATCACAACTCAAATATAAAATAACCTACAAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGTT GTCATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTGTTGTCATTTTATTCTATTG/A/CJATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTTAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTACTCTGGTGATGCAATTGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTTAAAGAGGACTATTCTTTAAACAAAGACAGTGTGACATTATTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCATTTGAGTCTTTATTATATTGGGAATTGCAGTGATATTAACTTTGTACAAAT GCACAAATCTTGCTCTCTC/TJATGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGCTCT AATGAACCTCATTGTCCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA G A T T T T	TGCTGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTTTCTGATATACATT/CJCATCTT ATTCACCACGAGCACACACACGACAGTAGAACAGTTCACACCTGATAAATTGCACAAGATG
WI-14482	17	G A ---		---	GCAGAACCAATTAATAA/G/AJAATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---		---	TGTAGTCTTCAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATTCOCAGTATCATGTAC GCCTAAATAAAT/CJGTGTGCTTGTGCTGCTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A G T C G C	TGAAGATTAA CCAGAGTCCG C	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAGTATACAGATACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCCG/C/CTCTCTCAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA A T G T	CTCCAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTG/TJACCT TACTATCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---			---	TCCTATTACAGCCAGAAATAACCCAAATTATTTCCAAATAAGCAAAAATTGGAACAGACTGGA GTGAGAAACGAGAGTTCCACACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGCTTGGGGT GCATTCTAGTGGACTTTAT
					GTCAACATGTT ATATTTTCTTT TAAGAC	TGGTACAGAATGTTTAAATTACAGCAGGGCAGTGATCCAGTTAAATAAAATTAACATGGTGACAGCTTT CCCAAAATATAAAATTAATAATTAAATATTTAAAGAAAATAATAACATGGTGACAGCTTT TCCTTAATTTTATCGGAATCCAGGACACACAAGAAAACACCCAAAACACATGGAGACAGAAG ACGAGACACAACCTCTCCCCACATGCGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C ---			---	TCCTTAATTTTATCGGAATCCAGGACACACAAGAAAACACCCAAAACACATGGAGACAGAAG ACGAGACACAACCTCTCCCCACATGCGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---			---	TCCTTAATTTTATCGGAATCCAGGACACACAAGAAAACACCCAAAACACATGGAGACAG AAGACGAGACACAACCTCTCCCCACATGCGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G G G A C A C A A	TCGGAATOCA	TGGTTTTGGG TGTTTTCTT		TTTTCATTATTTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAAATGTTGTCATAATAATAATTCATATTCAGGATTTTG TGAAATAGGTGATGGGA
WI-15116	96	C T G T T G C A G T A A	GGGAGCCCTA	CCTGAATATGC AATTATTTATT ATGACA		GCAAAGCAAAGCTATGGAGCCCTAAAGGAATGGGAAATGTTGTTGGTGGTGGCTTGATCTTGGT GCTTGTGTCATGGAGCAGAGTCTCTGTCATGCGAGGGCGTCACATATTTTAACGCACTAAT TTGGCAAACTGTCATTC
WI-12578	37	C T A A T G G G A A		TCAAGCGACCA CCAACAG		ATTCACGTTGGCCAGATCTCCCTTATGTTGGCATTGCAAGAGACACTGCACCTATCTGAGGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTTAGCAAGGCAAAATACCATTTCCTAA
WI-15153	40	A G G C A T T G C A	CCCTTATGTTG	T		CCCTTGCTCTGAACTGGGACCAAGGATGTAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAAATGGGAGCTGACTTTTCCCTGTTGGTGGAAAACCTCTGTGAGGGTTTGGCA
WI-15215	84	G C T C A A A T G G G	TGGCTTTAGAA	CCAACAGGGGA AAAAGTCA		AGGAAAAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGCACGACACTTGAGGAC CTAGAAAAGCAAAACCTGAGGTGATTATGCCAATCAAATGCAAGGTTGGAGATATGCTAAAA
WI-15225	80	C T C	CTTGAGGAOCT	TTTGATTGGCA TAATCACTCC		AATTTGCTAGTGCAATGGACCCAGAAATGGAAGGGCTATGTAACTACACAATGATGCACACCAC AGCCATGTGAGTGCACAGATCCTCTTGTCATTCAGCTTCTTAAACACATCAAAGGCTGCA
WI-15152	51	G A ---		---		TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATGCTGTGCTGTTT GCCCTTAAGCAATTTACAACTCAGTGGGGAAGAAACAGACATGCAAAACGAGATAAAACACAAT
WI-15123	55	C T T A G G A T G	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACAGAC		

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACCTAGCTGACACAACAGGGGCAAAATAC/ATGTCTGGATTAAACCCG ATGCTAATGGGTACCTTTATTTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGCCCTGGC ACTATG	ACTTATCCGTC AGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTGGCCCTGGCACTATG/C/CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTACAGATTGCTTGCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT TGAT	GTGTAGTCTT ACATGCTTAGC TAGAC	TCAAGTGGTAAATAGCCATTATTGAGTATTCTTGCTTTGAT/C/CTGTACGTAAAGCATGTAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGAAAGTCTGGTATTATGGAAAAACATTTTGTCAATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATATGCCCTACATATTTAGTGAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGCTTTTGTGGCAAAATATGCATAACAAAAT/ATTTGCCAGTTTAAACATTTTCAAGAGT
WI-15239	57	T C	CATTGCAAT AACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTT/C/CTGCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCTGCTGGTTCAGCTTCCAGCTTCCAGCGAGT
WI-12634	52	T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTAT/C/CTGCTATTAGCTA TGTTTACAAATTTGCTCGAAGGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATTCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTT/C/CTGTAAAAATCTCTGGCTTTCTGCTGGTGG TGAGGAGGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCGAG CCACATCTTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAAATGC	CCCTCTCCTCA GTGCACIT	CTGTCCGGGGAAGACACCGTGCAAATGC/C/TAAGTGCCTGAGGAGAGGGGAGGTCTGTGACTC CCAAACCTCGAATATTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAATGCTAGTGGCATTAAAGATGC/AG/CTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTTACTTGGATTATCTCAGTTAAAAACCCACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/G/ TJCCATTTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGGAAATTTAGCATAATTTCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTAAGTGAACAAAGGATGAAGCT AATCATGGA/G/AGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTA TCCCTG
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGTTTAAATGGACTCACAGTTCCATGTGGCTGGAGGCT/C/CTCACATCATGTGTGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123	C T	AGTTGGCATT AATAGCCTAT C	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTATCCATGGCGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC/C/TAACCTCCATGT GGGAGTTTCATAATAA

WI-14528	62 T	T T T T A A C T T T T T C T G G A T G G T A T A A A T	C T C G A T T A G C A C T T A T T A T A A A A A T T A A A	T A T G C T T T A T T G A A G A G A A A T A G G C T A T T A A T A T A T T T T A A C T T T T T C T G G A T G G T A T A A A T T / G J T T G A A T T A T A A A T T T A T T T T A T A A T A A G T G C T A A T C G A G A C A T C A C T G G G T A T A A T T G A
WI-15347	74 C T	G A C T T C A A A G G A A A A G A A C A A A T T	T C A C T C C C C C A A G C T T T G	T A T T C T T C G G T T C G G A T G C A A A C A A A A A A T T T T A A A A G A A A A T G T G A C T T C A A A G G A A A A G A A C A A A T T / C / J C A A A G A C T T G G G G A G T G A A G G C A G A G C C T G G T G C A G A T G G A C G A G G T C T G C A G A C G
WI-14546	95 C A	C C A A T T T C T A G T G A T A G T A G A G G A C T C A	A A G G T G C A C G T G C A G G	G T A T T T C T G A T G C T T G A C A T C T G G G G C A T T G C T G T C T A G A G A G A C T A C T T C T C T G G G A C C A G C C A A T T T C T A G T A G A T A G A G G A C T C A / C / A C C T G C A C G T G C A C C T T T C A T A T A C A G A T C A
WI-15353	37 G A	---	---	T T A T T G G C T G T C T C T G T A T A C A A T G T G G T G A A A A C / G / A / J C T T A A T T C A G G A C A T C T T C C A C C T T G T T T G G C T T C C A G T T G T A C T G C A A G A C C A G T G T C A G G C A C A T A G G C T G A T T A A T C A G T G G
WI-14580	100 G A	C A T T C C C A T C T G T C T T G C A	C C G A C C A A G A T C C C T C C	A G A A T T T T T C C T T T T T A A C A G G A C A A G T A A C A G A T T A C A T C A A A C T T C A G A A C T T C T C A A A T A C C T A G T T A T T A C A C A T T C C C A T C T G T T G C A / G / A / G G A G G G A T C T T G G T C G G C T T A A C A
WI-8540	73 T C	G G C C T G C A T T T G G C T T A	G C C C T T C T T T T T C A G G C A C	C C A G C T G G A G T G G A T A A A T G C G G C A A C C A C A G A A A A A A C A C A G C T A C A C A G C C C T G C A T T T G G C T T A T / C / J G T G C C T G A A A A A G A A G G G C C G A C C T C T T G A T A A A G A A T G T C T
WI-8039b	97 T C	---	---	A A G T A G A A C A C A A T A G A A T G G C T C A A A A T A T C A G A A T G C A C T A C G C A C A T C A C G A G T A A A T A C T G T T T G G T A A A A C T T G T T C A G T T / C / J A A A T A T G T A T G T G C C G T G C A T G A T T A A A T A T C C T T C T
WI-8039a	87 T C	---	---	T A C C A C A G T C A C C C T A A A G A A C C A A A G C T T A G G A C T A G G G A C A C A A C C A T G C A G A A A G A G C A G G G A G A C C A G A C A C T C T G G G T T G A G A T G A T T T A A T G C C G C A G C C G A C A C C C A C A
WI-8044	107 C A	---	---	C A C A C A T T C A G A A G T T T T C T G C A T T G T G T C T T C T G A T G T C T A A A A G A T T T G A G C T T T G A C T A T A C G A T T T C C C A C A C T G A C G C A T T C A T A A G T T T C C C C / C / A / J A T A T G G A T T C T G A T T A A T A A G C C C G A A T T C T G G C T A A A G G C T T C C C A C A T T C A A G A C A T T T G A A G G T T T T C T C A G T G T G G A C T C T C T G G T T G C A C A A G A A T G G A A C T T C G G C T G A T G C T T T C C C A C A C T
WI-8550	32 G A	G G G A C A T C A A T G C A A C A A G	T T T G T G G C T T G A G T T T A C A A A T T	C T T A C T A C A T G G G A C A T C A A T G C A A C A A G T A / G / A A T T T G T A A A C T C A A G C C A C A A C T T A G T T A A T A A T C A T G G T A A G G G A C A T T G C C A A A G A G C A A C T G A T G C C T C A G T G A A
WI-8057	87 T A	---	---	T A T T A G A T A A A C C C T T T G T C C G A T T C A G G A T G T T A A T T T G C T C T T T A A A C T C T G T G A C T T T T C C T G G T C A A A A G G A C A G T / A / J A T G G A C A G C A G A G A G T G G G G T C T G A A A A T G T A A T C T T T G T G T C A A G G C A C T C T G T G C C T C A C A A C T G C C C C C T G T C A G A G G A T G C T G C C T T C C A G C C C T A A A G A C A C T A G G C C T T T C A A T G G A C G G G G T T T G A A G C A G C C A G A T G T A A G G

WI-6192	91 A	GAT	GACTGCTAAG GATTTAATTTG	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGAACAAATTAGCTCAGTCCAAACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTGGATTA/GIATTTTAATACTTAGCCATCTAACACTTCAAGCATAAAC
WI-6194	105 T	A GAAA	CACATGGCAA TGATAATAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAATAACATTTCTCAAACTCAAACATCATGCTTGAAATATCACTGAACTT GTCACAAAGAAAGTCACATGGCAATGATAATAAGAAAT/ATATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAACAAATGGAATTTGGAAAAATAGGAGTAAA
WI-6213	164 CT	---	---	---	CATATGCTGCTTTATTTCTGTAAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCCTACAAGAAATGTTAGTATGTATTGTCTATTACATGTTT ACTTTTGATATTGCTCATTATCTATGTC/TATATAATAATGTAATAACAGTAAGTAGGTGATCC TGCATTTCAAGTAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
WI-6217	131 CT	---	---	---	CGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCAGGGCTTCAGGGCTTGACAAGCAGCTCATTCAGG[CT] GGCCACCATGGCCCTAGGGTCTGCTCAACAAGTCCAGCAGCAATCATGGGTTCTCGTATATCTGATCC AC
WI-6238	175 GA	---	---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCCTCTGTTTGTGTTTTATGCTTTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTTGGTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTG/AGTTCAGACTTCAGGAAAATGATT TCCACATGGTAAGCCAGAGTCTCCAGTGTGGTTCATCCAGAAAGCAGCTTG
WI-6272	86 CT	TAA	GCATTTATTC GGGAAACTT	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATAGTCACTGTCACAGTCATAATAATGCATTTA TTACAGGGAAACTTTAATTC/TJTTCTTCTTCTCAAAAAACAGCTGCTGGAACACCTCAAATTA GGGATGTTTCATCTAAACACCTTTACTGAACTTGATTCCTTGGGOCAGAGGAGGCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTTCGGGCAATAAATGAATACTTGATGCATTTCATACAGGCAAGAA TCCAGCATCCAGAGAAGCTCTGTGCTG[GA]CTGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCTCGATTTCCTGCCAGCAGTCTCTCTCTCTCTCTCTCTCTCTGCCC TCTG
WI-6303	96 GA	CTCTGTCTGC	CCCAGAGAAG	CAGCCATGGCT TTGCAG	ATGCTTTTGATGATTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGTCATGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGCTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGT[CT]TCTGGTT CTTCCCTTACATCTTTTGGGGA
WI-6315b	193 CT	---	---	---	ATGCTTTTGATGATTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGTCATGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGCTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGT[CT]TCTGGTT CTTCCCTTACATCTTTTGGGGA
WI-6315	187 T	C---	---	---	CTTCCCTTACATCTTTTGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGAAATC	AATGTGAGATC TTTATTCTAAG CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTTATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T G C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGTTGATA	TCCTTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTCGTAGTTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAA[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTACATGGGCCTATTTATTAGGACATTTGTGTAATGTTCCACTTTGTTTAA [C/T]AATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTACATGGGCCTATTTATTAGGACATTTGCTGTAATGTTTCCACTTTGTTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA[T/C]AGGAATGGATGCTGTGTCAGAACATACTGCCAATAAATCTTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCAGAGCGGATGTAAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C G T C A T A	TCCTTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTCTCTGTCCTTT TTACTTAGCAAGGAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCATTTCTCAAGCACAT T/CJACCCAAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGGGCCAAAGCTATCTGGTTATATTTTATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACTTATTAAAGGAGAGTACTAGGAAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAATATAGCTGGTCTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG	TAGCC	



WI-6690a	28 T C A G A G	A A C A C C A C C A T T A T T A A G G	G C T G T G T T G G T A G T T T T C C T	T G C T A A C A C C A C C A T T A T T A A G G A G A G T C / A C T A G G A A A A C T A C C A A C A C A G C A G C A T G T G A A A C A G T T G G C A C G G T G T A A G G G C A C A G A C T C T G G A G C C A C A G C G G C T A A T A C A C T G C A A T A T T T T A T G T T A G C A A A T T A T A G C T G C T G T G T A T A C C A G A A G A G C G G T A T C T G G
WI-6770	53 A G	C A A C C C C A A A A C A T C A C A	G C T T T G G A G T G T A T A A T A G T A T G A A T A A	G A T G T T A A T G A C A C A G A T C T T C C C A A G T A A T C C A A A C C C C A A A C A C A T C A C A / A / G / A A T T A T T C A T A C T A T T A T A C A C T C C A A A A G C A A A T A C T T C A A C T G C A A T C C
WI-6686	151 A G A	G C A T T C T T C C A A A A C A A A G A	C C T T G T A A G T G A C T A T T C C A A T G T T	A T T C T G T A G G C A A A G G T T C A G C A A A T C A G C T A G C A C T A A T C T T G A C C A A A T G G T G A G T C A G C C T C A T C A C A G A G A T T T T T T T A A T T A G A T G A A A T T C A C A T T A A A A C A T G G T A A C T C C A A G C A T T C T T C C A A A A C A A G A A T / A / G / A A C A T T G G A T A G C A C T T A C A A G G A C
WI-6761	32 C A G	G A T C T A A C A G C T G C A G A A T G	A A A G C T G G G A A G G A A G A A G	C C T G A G A G G C A G A T C T A A C A G C T G C A G A A T G G / C / A / C T T C T C C T C C C A G C T T T T G T G A A C A A A A C A A T T C T C T A A G G C A T C A G A A A G C A C T G A G T G C A A A T G G G T T G T T C A G G T A C A A G G T C T C
WI-6844	225 T C ---	---	---	T A A A T A C T G C C A A C T A G C A T T A C G T C C A C T C T T G C A T C A T T A A A A C A A A G G G T A T T C C T C C T T G G T A T T T T C A A A T G A T G C A T T A C A A T A A C G A A G T T A G A A C T T A A A T G C A C C C T G A T T A A T T A T G T A A C T G G T A A T T T G T T T A A A A G C A T A A T T T G T T C C T T C T C A T A A A A T G G A A A T T T A A A T A T T C T C T G A T A G C T T G A G G T T / C / A T C A T T A T A G A T A G T G C A A A G T G T G
WI-6824	112 A G ---	---	---	C G G T T T G C T A C A C T T A A T G G G T T T T T T A A G G G A T T T T T C A G G T C T T G T C A G C A A C A T C A A A C A A A G G T A C T A G T A C T C C A C A G G T A C A G A G T G C T G C C A A / A / G / C A C C T T A G A A A A A T T A C A T G A C A C G G A A A A T G C C C T T G C T C T T G A A G A G C T T A C A G T C T A G G A T T T G A C A A C T C A C A G T C T T A G G A A C T G G C A A A G T A A G G C A A T T C T C A T C C C C T A G A G C T A T T G T G
WI-6889	139 T C A A T T C	G A A A A A T G A G A T G C A G T T A A	T C A C T T T G T G G C T T T T A A T T A T T C T	G T A C A A A A A A G C T G A G A A G C C A A C A T G G A A G T G T C A A G A A A C A T T C T G A T A G G T A C G G A C A A A A G A G C T C T T C A A T C A A A A G G A G T T A C A T A T T A G T T C T C A C C A T G C T A G A A A A A T G A G A T G C A G T T A A A A T T C / C / A G A A T A A T T A A A G C C A A A A G T G A A A C T G T T C T G G G C C C T A T G T T G T A G A T T C T C T
WI-6911	216 T C ---	---	---	T C C C A G C T C A T A T T T A T T G G G C A C A G A G T G G C A C T C A A A T A T C T G A T G A A C T T G A T G A A C T G A A A A G A G G T C C T T A A C A A G A T A T C A T C C C G A A G A G A G A G T C C C A C C A T A T A A A A T G T A T G A T C A A G T C C C A G A A A C T T T G C C T C C C A A G G A A T G T T T C T A A T T T G G T T C A A A G C A C A C T G G T T C C C A C T T T T A C C A C T T / C / C A T G A C A T T G G A C A A T A G T A C T A C T C T T T C T A C
WI-9413	112 G C ---	---	---	G C C A G T C T C T A G T A A G T C T A G G G A C A T G A C C A G A C C A G A G C C C T G T T C T A T A T A G A C A A A C A G G T G G C C A T A C T T G G T G G A G G A T A C C G T G T A T C C C A G A T / G / A A G A T T G G T G G A A G G A G A C C A T G A C A G A T G A C A A A C G G A A C A G T T T C T C A A A A C A G A G G T A T G A
WI-9557	74 C T ---	---	---	A A A A G C T T T A A A A A A A A A G T G G T G C T A T C T T A G A A A C A C T T C A G C A A G A T C A A G T A G C C C A G C T A C A G C C T C / T G G T G C A T C T T A A C C C C T C T C C T T T



WI-9617	37 G T	---	---	TGCTCTTTTATTTACAGTTTCAACAACACACGCCGCTG/TJGGCACAGTCTACCAAGTGCCCGCAG CGCCACGCTGGCCGGAAGGCTCTCATCTGTTCTGCTCTATGGACTGATTGAATTTGGGATGGCCAG CTOCAGAAATGTTCCACGTGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTTGCCACACTGGCAACA AAGAGGTTGCACGATGCAGCTTGCAAGTGGGTCCAAAGCCGGGTGCTGTG
WI-9657	121 T G	---	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCCTT TGTAATAAATAAATGTTTATAAATGTTTATGAAGCTCATACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C	CCTCCCAAGTA GCTGGGA	AAAAATTAAC CAGGTGTGGTG T	CAGGCTTGCTCTGTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGCTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC
WI-13119a	51 C G	---	---	CAGGCTTGCTCTGTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTTC/GJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTTGTAAAGATAGGCTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
WI-13112	71 C T	TCATAAAGAC TACAGACTTA AGCTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTTG/CJCTTTTCCATATAATACACAAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAAATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36 C A	TGGTACGTGCT CTCAGTACAA GTTT	CAAAGTGTA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACA/CJAAACAGCATCAGTAGTGACACTTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAGAAAGCCCAAGGTGAGAAAGTATAATGAATATGTACAT CTTTATGGAAAGTGTGTTGTGAGCCTCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-13020a	108 G A	CTAATAGTGG AACCCTGAGA CTTT	CATTATTAAAC CCCTTTCAGA	TGCTATTTCATGACAGACACGTCGAGACAAATATTCCTATTTTACAGATGGAATAGACCCAGACATT TTCAGTACTTTAACCACTAATAGTGGAAACCTGAGACTTTA/GJATCTGCAAGGGGTTTAAAT GCAAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTTCCATTTTCTTAAAGAAATGA TAAAAAATGTTTCCCAATAT
WI-12837	87 A G	CCATATACAT ATATCAAGGT AAAGTCCA	GCCATAGGAA ATGCTGTTTT	TGTATAAAAAATCCAACCTGTTCACCAAGTACATATGCTCTATGATTTTATGCATATCATATAC ATATATCAAGGTAAAGTCCA/GJTACAAAAAACAAGCATTTCCCTATGGCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTGTGTCCA

L42611b	50 GC ---			GTGCTCAGGCCCTTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCCTGTGCGTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTCCCTCAGCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGATTTACCA
L42611	34 TC ---			CTGGAGCTTCACCTTTGTTAC GTGCTCAGGCCCTTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCCTGTGCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTCCCTCAGCTTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGATTTACCA
WI-1172b	179 CT A	TGAAGAAATG GCTGATAOCA	ATGTGCATTT TCACTGCAG	CTGGAGCTTCACCTTTGTTAC TGAACGTGTGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCAGATTAATGTTCTTGAATACCAATTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 CA ---			TGAACGTGTGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCTAGAAACAGTG GTGACCACACCTCAAGCAATGATTATCCCTAGCAGATTAATGTTCTTGAATACCAATTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 GC A	GCAGATTGGA AGTGTAATA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCAG AAATGTAAAGTGTGCGCTCACTGTTCTTACCCACTTAATCTGCAATTTTGAACACTAGATTGAAT TCCCTTGCAAAACCTTGTCATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACATGG CCTGGTG
WI-1231b	141 GA ---			TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCCTCTCTTCAATTAATTTCTT TCAC[G/A]TTATTCCTCAGCCTGAACGCCCTTCTCCTCGTAGTGACATTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126 TC A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCCTCTCTTCAATTAATTTCTT CTTTCACGTTATTCCTCAGCCTGAACGCCCTTCTCCTCGTAGTGACATTTAAATCCACTTTACA CATTCGGACC
WI-472	114 GC ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATAGATATCCATTATACAAACAGAAAAAG[G/C]GGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG TTACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTACTCTATTTTGTTC/CTAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATAGTCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
WI-533	29 T C A A C T	ATCACAGCAG AGTACCTTTCT	CCITCCAACCT CTACACAATCT T	AGCCATCACAGCAGATACCTTTCTAACTT/CATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTCTGTGGTATAATGACCTGTGTCCAGTTAATCCA TCAGTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCAACAGAGAGGTTTCACTTGACTCTCTAACTGAGTAC/T/CAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGTGAGTACAGGAT
WI-601b	112 T A ---		---	TCAGTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/T/AGAACAGAGAGGTTTCACTTGACTCTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGTGAGTACAGGAT
WI-601a	74 C T ---		---	AACAAAAACAGACACCCCTGGCTTCTCTACCAGTCCACATGGGTGCCAAACATCCACACATTCCT ACATCTCCCACTGGCTGCCCTCTTCAACACCTCACCA/AG/ACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTAATGCAACATGGTCTGGTGCATAC
WI-863	107 A G C C T C A C C A	CTCCTTCACAA CCTCACC A	CTTCCCGTAA GCCAAGT	ACTCACTGCTTGTGTTGATTAAATCAACCTAGCC/G/AGCTGTCATGTGGGATTAGAATAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37 A T ---		---	TGCATTCAATTATGCACCAATAATAACTTCTGTACAT/AT/CATTATTGTATTTCATTATCACAAAT TATGAGTGAGGGATGATTGTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAT GTTCTGCATCACTGTACACACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C C C A	CAGTATCTGA AGTTTTGTCT	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTGCAGTGGATAGTGTTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC A/G/C/JAGAAGTCAATTTGTAGGTCTCTGGCGTTTGTCTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTGCTGCTGACTGACTGAAG TTTATGCAGAAGGTCCATGAGTTACAGATCTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGATGGCTGTCTCATGAAATTTGGACAGCATGTTCCAGAGAGGAGGAAACAGCATGGAGAAGA AAAAATCATCTATCCACGTGCAGAACTGGCAATAGTTTTGT/AT/TTACTAAACACAAATGT TTAACTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5381	178 A T ---		---	CTATGTATCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/G/ATCGAAAGGAAGTTCTATGTCCATAGACCCCTATCTCACTGACCCCAAGGTA AAAAAATAAAATAAAAGTAAAGTAAGAACTTACATCAGATTGTGCATTTCTTATTTTGGCCACCCTGTTGT TAGGAA
WI-5791b	76 G A ---		---	

WI-5791a	44 C G ---			---	CTATGTATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/GJACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGCGCATTTCTTATTTTGGCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			---	CACTCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGOC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/CJ/CTTATGAGCCAC ACTTCTCATTTCTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACTCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAG TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/CJ/CTTATGAGCCAC ACTTCTCATTTCTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAGAGAGGCAA GG
WI-5406a	42 A G ---		---		CACTCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATCTGTC TTGTTTCTTT	ACTGTTAGAAA ACCGATATTTT TCAAT		CCATTCTCTCTCCCTCTCCCTTTATCTCCCTGTTTCTTTTG/CJ/ATGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT		CCTGCTAATAATAATTTAAGCACGATTGTCTTCATGAATTCATCTTTCAGTTT/T/ATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG/CJ/CTTAAACCATATTTTGTGTTTA GAACTCTGTGGCCAAACCCTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTCG	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGCATCTGTTTCAAC TCTCTGTTTTCAGAGAGGTAGTATATGCTGAAAAATCTATTTTGTGATTTATGCTGCAGTCG/JA/GJA ATACITGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29 G A AATTT	CCAATTTTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTG/JA/AAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTCAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACITGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38 T C ---		---		TCATGAGTCTTCTTCAAAGATGCTTGTAAAGTCCCA/TG/JCAAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACTTAGGATATTTTGCAGACCAA

WI-5826	134 T C ---				<p>TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT  TTTCACITTAGTTAAATGCTTTTCCCTTGATGATGCAATGGCCAGTTTATACATATTTCTTTAGTC/C  TTCAAATTAATGCCACCATAGAAATAATTTTCTAACCAACGAGCCAAACAGCCTCACTCTTCCCTT  CCTGGTGCAITTACTCTTTACAC</p>
WI-5546	40 C T A	CCCAATACITTT TTCAGGTGAA		CCTGTATTTTA GCAACATGGG	<p>CCTTATAACCCCAATACITTTTTCAGGTGAAAAAGGAAAA/C/ACCCTATGTTTGCCTAAAAATACAGG  AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATCTGATGTGGGAAATAT  TAGAAAATTAAGCGAGAGAGGCA</p>
WI-5552	97 C T	GGCACCAGCCT TTTTAGAGT		TGCACAAATTG OCCAGG	<p>TGTTTGTTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGATTGAGCGGGTATGGGT  GGGGCTATCGGCACCCAGCCTTTTAGAGTC/TCCTGGGCAATTTTGCACACTAGTGTACAG</p>
WI-5836b	161 C T ---				<p>TAAGTTGATTTAAACACTCTGTGCCTCAATTTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA  AAAAGAGAGAGAAATTAAGGTGGATAGACATGAATAACTCTGATGATACTGTTGTATCCCTGAA  TCTGCAATATACACATGATTCAATGAT/C/TCCTATTTGAAAAATTAAGCTTTTGAATTGTTTCCCA  ATG</p>
WI-5573	58 C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC		<p>TCGGGTATTAGGATCGTTTCAACCTCGATGATGGCGTTTCAAGGAGGTGGGA/C/TCGACAC  ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG</p>
WI-5850b	134 G A ---				<p>CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTTCTCTGCTGCCCATGGGTGGAGC  CTCTCTCAGGCTTCCCTATGACGCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTC/GA  TTTTGCCATTTCCGTATATCAAAACAGAGAGAGAGGGTGG</p>
WI-5850a	92 C T ---				<p>CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTTCTCTGCTGCCCATGGGTGGAGC  CTCTCTCAGGCTTCCCTATGCA/C/TCGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG  TTTTGCCATTTCCGTATATCAAAACAGAGAGAGGGTGG</p>
WI-5612b	125 A T TTC	CTATTAATGA GCATCGTGTC	TTCTCTTGAGA AACCTAAAAC ACTG		<p>TGCCTGATTGACACATAGTTATCTGACAGTAATCAATCTAACATCACAATAATCTTTTCTGCCTG  TCACACTAATTTGCAAGCAATCAATGATTGACTAATGAGCATCGTGTCTATTGATTCAGTGT  TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTCTGTAACCTCAAGTA</p>
WI-5612a	44 T A ---				<p>TGCCTGATTGACACATAGTTATCTGACAGTAATCAATCTAACAT/A/CACAATAATCTTATTTCTGC  CTGTACACTAATTTGCAAGCAATCAATGATTGACTAATGAGCATCGTGTCTATTCACAGTGT  TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA</p>
WI-5636	26 A/C	GCCAAATTTAT CCGCAATAA	CATCGAGGACT TTGGGA		<p>TGAGAGCCAAATTTATCCGCAATAAA/C/TTCCCAAAGTCTCGATGGAGGCATTTCAAGATCGGG  GCAGGGAGGAGGAGGAGGAGAGAGATGTGAAGAAC</p>



WI-5967	165 CT ---				GAGTTAATGAATCCTGTTCCCTCCTAAACCCCTCTGTTCCCCCAACTTCACATTACAGAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCCGTATCTGTGCTCCAATCACCATTCCACATTTATTTCTTATAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53 GC ---				GGTGAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACATTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAAGGAATGAGG
WI-6141	80 TC AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAATAAATTGAATAATTAAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTATCTGACTGTTCTGGGGTTTCAATCTCTTACCTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTTACATGCAGAGAAAAAGGGGAGATAAAAATTTGTCTTTT CTC
WI-6450	45 TC GTGCACA	CCAATGACTT ATTCTATATCT		TTGTTTGAAT GTGTGTACTT CT	ATAGGACAGTTTCTTCCAATGACTTATTTCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAGAGCCAGGTATGCCAGGTGGGATTTTTCACGGTCATGTAATATGCATGAAGACTA TTTTACTGGCTTCTTTATGCATAAACCAAGGATTTGGTCTATTCACAAACATGTGTCAATACAG CAGTTGTCATGTCCCTCTGTGCTACTAGATATAGTCTTTATAGAATATGTGTTTAGAATAAAGCCACA AATTATCTATAAAACAACA/C/JAAGGAACGAGGCTCAAAAGTGAACAACAAACGGCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-6461	88 CT ---				GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTTCTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCTTATTCAGTGAAGTATGATCATAAAAGACATGCAAAACCTTTTCACAGTCTTG CCTGG/GAJAATATCTCACAAAATTAATTATAAATTTGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCTTT
WI-7466a	141 GA TTTGTCTGG	TTTTACAGTC TTTGTCTGG		AGTCGCATGCC AATTTATAAT	GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTTCTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/GJATTGAGTGAAGTATGATCATAAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATTTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCTTT
WI-7466b	80 TC GTC	GACTTCTGGG CTATGAAATA		TGCTCTTTATG ATACTAGTTC ACTGAA	TGCTTTTAAAAATAACAATGACCACCACTGACACCATAGTCTGTCTCCATTGGCCAGTCTTCTC AGTAGAATAAGACAGGACTTTGCTGGTGTCTATCTGATTTCTCTTCCAGAGAGACTTTGGCCCT CATAGGCATTCATAGATATTTGTTGAATGAATGTGCTTTTGTCATATTGATTCCTACATTTGATACA TTCTCAGGAGGAGACTTTGGCTAT
WI-9814	104 CA ---				CCTCTAACAGAAAACTTGACTTCTCAACTCAAAATACCTTCTCTAATAATTT/GJAGTAACCA AAATATCTCTCAATAAAATTAATCTTTAATTAGAAGAACAGCAACAGTTAGAGGTAGTACATTCA CCAC
WI-9720b	55 AG ---				

WI-9720a	47 A G ---	---	---	CCCTAACAAGAAACCTTGACTCTCCTCAACTCAAAATACCCCTTCTCTAGATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	---	CACGCTTAAGGCAGGATGTGGCTATGAGATACCTTTGCAATTGCTGTGTCACACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCATGTCAGATGAAGGCTCAGGGTCTTATJGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTACAAGAAGAACTCACAGGGTTAGTTTGCAAT TAAGAATTGCCAGTCTTTGTCTGTCATCATCTTGAACATTATCCACATG
WI-9748	74 C G ---	---	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTCTAAAGATTCTTAATTTTATATGTTTACCCCTT GTCATTGCTCAGACCAAGTACATGTTTCACACAGCCATCTTCTTTTCCCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCA
WI-9943	91 T C ---	---	---	TGAGGCTATGATTCAGATTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTTTATATCCATCTTC/CJATTTTAAATTTCTACTGAGCAGAAATAAATGTATACATT AACCTTGTCTCCTATTGTACCTTTTAAATGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C ---	---	---	AGGGCCTTCACAGATCCGTGAGTCAACACTGCCTCTT/CJAGTGAGCCTGTGAACCCACCAAGAC GGCTGGTCATCAGTGTATCCTCTCTCTTCCGGACAACTATCTTTAAAGAAAAAAGAGTGT CTTGAATGTATCCATTTATCCCAATAATCTTGTTTAAATTCCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCAATCTACACAAAGGATTGCAAA
WI-9897b	84 C T ---	---	---	CTCAGAAATTATTCAGATCTTCCCAATGTCATGATTCCTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCTAGCCTGTAT/CJAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	---	CTCAGAAATTATTCAGATCTTCCCAATGTCATGATTCCTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCTAGCCTGTAT/CJAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	---	AGATAACCCCTGGAAACTAGAAGAAATTAATAACGTGTGTCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACA/CJAGCCAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATA
WI-9935a	42 C T ---	---	---	AGATAACCCCTGGAAACTAGAAGAAATTAATAACGTGTGCA/CJACCTCACAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATA
WI-9983	146 C T ---	---	---	CCGTGTTAGTGCCAGAGTCCATGCTCTTGGCCACAATGTAGGCTGCCTCCCAATTCCTTTGTCTTGA TTCCCAACCCCAAGTTCTCACCCCAATCTGATCAAAATGCTGACTAGGTGCTGCTGCTGAGGTTAA AGCATTATGA/CJTAGACACAAAGACAAAGAGGTTAAAGTTGCTGCTCAAGAGAGAGACATATA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG



WI-10019	139	A T A T C T	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTTGGTTTATTTATGTGTGCTATAAAATCAATGGTTCTA ACATTCAAATAAGATCTTTTGGTCTCTGCTCAGATGCTTCAATGATGTAATGCTATGTAGCAAAAT CTA/TJCCCTAAGCACAGTAATCAAGGCTTCTACCCCA
WI-10020b	122	T A T T T	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTJAJAAAAATACC AGACTAATGATTAAATAAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A T A A A T T	TGTCATCTTGA CTCGTATTAA	AAATTCITTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATATJ/CJGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAAATAAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10084b	170	C T T T T A C A T G	CCTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/J]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10084a	54	C A C A G G G A A G G	GTAGCAGGAT CAGGGAAGG	CAAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATAAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTAT TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C C A A A C T C T T	TCTCTGTGCC CAAACTCTT	ATTCTTGTTGT ATTGAATGBAA TTAA	CCAGGGAATCTCCTGTGCCCAAAGCTTATJ/CJTTAATCCATTCAATACAAGAATTTATAGAA TATGCACCACATGCCACAAGACACCCCTTATATTAGT
WI-1319	40	A T A T T C T T T	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCCTTTJATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAACATTAACTGGTGCAGATGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T C C T C T T	CTGTTGATTTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGGTGACAACTTAGTGAGGTGTAATCAGAAGCATCTATATTATTCACAGTCACCAACCTG GACTATAGTCTGTTGATTCTACCTCTATTCTCTTAJ/CJTAACCTTTTGGATACATTCCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T ...		---	AGTGAGTTGTGCACAATTTGGAGACATTCTGTGACCCCAACTTAAACACTTCTCTCCACACJCTJAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31	C T	TGAAGCAACC AGGCTCTGTT	CAAGATAATTAT ATTATTCTCT AAGAGGG	GAGGAAGCTGCCTGAAGCAACAGGCTTGTTCCTACCCCTCTTAGAGAAATAATATATCTT GAGATAGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTCTACCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCCTTCAGGG T
WI-10391	32	A G	CTGCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAAGTT GA	CCTCCCGTTCTCTGCTCAGGTATGACTCCCA/GTCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTCCAGGGGACGCATCTGACACAGCCTTTGCTTGTGTGACAAACAGAAATTCGAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146	A C GCAA	GTTACCCAGA GTCTTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGCTGACTTAGCGGGTGTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAA/AC/AGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82	A C	...	...	AGCGATGAAATTTATATGTTATGCTGCTGACTTAGCGGGTGTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60	T C	GGTGCTCAAT AAATATTAT	AAATTTCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGCTGACTTAGCGGGTGTCAATAAATATTATCTTTTTCATATT ATTTCCAATTATTAACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84	C G	CAAACTCAA ATTGCTTTAAG	AAATCCAACA GTCAAGGCTTT C	CGTTGGGAATTTTCTATCTCACCTAAATATGCGGTGATTAAATAATACATTTTAACAAACTTCAAA TTGCTTTAAGTACTTTA/C/G/GAAGACCTTGACTGTGGATTTTGTGATTTTCTTTTATTCTTAATA AAACATGCATATTAAAGTTGTCAGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33	A A	GGGAATATT TATCTCACCTA	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTTCTATCTCACCTAAATATGCGGTGATTAAATAATACATTTTAACAAACTTCC AAATTGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGTGATTTTCTTTTATTCTTAATA AAACATGCATATTAAAGTTGTCAGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125	T C	CACAAATGTA ACAAGAAATG	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCAATTTCCCTCAAAACCAGCTTAAATCACAATCAGCTTTTCTTTCCCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAAGAAATGATCCTATG/CJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C T	CAAGTGAATT ATGACCAAAA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAAGGAAACACACAAAAAGTTTCCCAAGTGAATTTAGCCAAAAATGAGA/CJTAAT TTGTTAAAAAAACCCTCAATGAAAGAGACAAATATAGTTCAAGATTTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGTGTGTTGGCAGACTTTTCTTTTCTTTTGTG/CJCTTTA GAATCCATTTGCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCAGCTTTTCT CTGTTGGATGATCAGGTTCTGCTCTCCCAATCCAGAGGAGGAGTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGGTGATGCTGCAATGGGAATATTGAAAAACC
WI-10656	59	T G	...	...	

WI-11169b	154 T G T T T T	TTAACCAAGA G T T T T C A T T C	CTAACTTAAAA A T C C T C A T T C A	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAAGTAGTGCCTTTTAACCAAGAGTTTTTCATCTTTTTT TTTAAAAAAGAGAGAGACAT/GJT/TATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G T T G A A A A A	AATAAGTGAA A G T A A C T G A C	AACTCTTGGT T A A A A A G C A C	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTTAAGCCT/GJA/AGTAGTGCCTTTTAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGAGACATTTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ---		---	CAAGTCTTGGACCTTGGATAGGTG/JACCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTATATAGATCTTGTTCCTTTTGGGTTTACCCTAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTGTCTAAATAATCCAAAATAGCCATGGGTTTGGACAAAATAC AAGGTAGTGTCTCTAATTAATGGGCATA
WI-10686	133 C T A A G G	TGCCCTGTGTC A A G G	CAATCTTAAA T T C A T G T G T A G A C A C A	AATAACCTGTGGCACATAAGGCAAACTACTGAGCCCATACAGAGTGTTTTATGTTAATATTGAAA AAAGTCAAGAGAACAAAGATAGTATAGTCTGTCTAGAACTTGAATCTGATGCCCTGTCCAAAGG C/TJTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
WI-11175	77 T A A	AAATGATCTT T C T G C T C A A A G	CTGTTCTCACA T T C T T T T T G A A A A	GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAAATATATGCTCCCAATGATCTTCTG CTCAAAGAGT/JTTTTTTTAAAGTTATCTACTTATTTATATCTGCTTTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAAGTAAGAAAAAGAGCCAAAT TGCGC
WI-10694	144 A G T A T G A G T T T T C	TGCAATGCTT T A T G A G T T T T C	GGCAATTTGTA A A G G A G G A A A	TAGAGAGGCTTTTTCAGTTTCAGGTTGGAGGGTGGTGGAGGTGAGATTCATCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAGAACTCAGTTCTAAAGTTTCAAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJT/TCCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT T
WI-2716	23 T C C	TGAATTCATCC A G A A A A A C A G	TCTCTTTCTC T C T T G T T G T C A T T C	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAAACAGAGAGAGAAAAAGAGAAATAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTTCTGTCTGCCAGTGCATGGAGCAGTG
WI-10719	115 T C G C C A T T C T A G	TGACTCTCAAG T C G C C A T T C T A G	GCACTGCCAGC A G O C	CAGGCCCAACTCTGTCTAATAGTGTTTTGAACAGACACCTCAGTCACACAAGTTTCTCTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCAGGCTGCTGCCATACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA A G C T T G C C A	GAACTCCAC A T A A A T A A A T C T C A	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCAJGJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTGAAGAGTTGAA

WI-11204b	88 T C ---				GCACGAAATTGATTATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAACTTTACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTAAATTGGGAAGAGATTTAGTGAATCAGAAAAATAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	GTATCACTTAA AATGTACATAA	---	GCACGAAATTGATTATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAACTTTT/AJACCTTTTATTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTTAGTGAATCAGAAAAATAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC	AAGAACAATG CATAACAGAA	---	ACATGATTTCCTTTAGTGGTCAGCCTTCTACCCCCAAGAAATATCCCTGGTTTATGCTGTCTTC ATTGGTTCACT/CJATTAAGTTCTGTATGCAATTTGTTCTTGAGTCCACATAGGTGTTAATCATCCCA CACCACCTGCTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	---	TAGCTTTTCTTTGTACGAGTGTATTAAGAAATTACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---			---	GAAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTTCAGATTTATTTAGT [C/T]ATTTTCTATAATAATTTCTTGTAGTGATGGATTTCTATAAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTCITTTATCCAAAGCCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT	---	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAAGAGATGAAAAATAGGA/GAJAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---			---	ATGAAAAATGCATTAGAAG/GAJAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GCGTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	---	AGCCACAGTGGGAATCATTTACACTACCGAAATCAGCAATGCTAAAAATTGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCCTGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGGCTG G/GATCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTTCACAGGCTACTGG AAAGCC

WI-1122a	25 C T A	G C A C A G T G G A A T C A T T T A C	T T T T A G C A T T T G C T G A T T T C G	A G C C A C A G T G G A A T C A T T T A C A C T A C T C G A A A T C A G C A A A T G C T A A A A T T G G G C T T T G G A T T T T G T T T T G T T T T C C A T A G A C C C C A C C G T T G A A C T A T T G T T A A C A T T T A C C A G C A T A C C A C T G C G G C T G G G T C A A A C T G G C T A C C A G G A A C C T G A C A G A C T C G T A A T G C T T T C A C A G G C T A C T G G A A A G C C
WI-10775	39 C T	T T T A T G C C A T A T T A A T T C A T T A C A C T C	C T A G A T G T A T T T G C T A A G A A A A T A T G A T G	T T G C A A G T T T G T T A T G C C A T A T T A A T T A A T T A C A C T C T C T A C A T C A T A T T T C T T A G C A A A T A C A T C T A G A C A C C T G G C A C T C A G T A A G G A T A T T C C T G C A C G A T A A T C A T T G T T A T C A T T A G A C A T T G C A G G A C C A C C A T A T G G A T A A A T G T G T T T A T A A G G C A A G C A A T T A T T G C A T G C A T T A T A C G A A G G A A T T A A A T A T C T T C C T A T A G T T G A A T T T A A G T A A A A A T A A A G T T A T A C A T A A T A C A A A A A G T T G T A A G T A T A G T A A C A A A T G A A T T A G A A A A T T G C A G T G G T T G C T A G T A C A G G A A T C A A A T T T G G A C T A T G A A C A A C T A G T T G C T A A G G A T A T T C C A C A A A T T A T T T C A T G A
WI-11226	165 A C	G C A A G G G A G G A A C A T T T A C A	C T G G T G A C A T C A G A G A T G G A C	C A G T G G C T G G C T A C T G A C A A A C G T A A C A T C G T G G C A G G T G G C A A G G G A G A C A T T T A C A G A G G T C C A T C T C T G A T G T C A C C A G C A G G G C C A G G A A G G T T G A T C T G G A G T G G G A C A C A C T G C T A G A C C C T C C C A G G G T C C C T C A A A G G T G G G T G T A G A G G C C C T A C T G C C C T G C C T G G G G A C G A G A G G C A T C A G G C C T T A G T C C T C T G G G A C A G T G A A G G G C C A C C A C C A C A G A A A A T G C C T A G G T C T T G T A G C A A G A G A G A A A G C A T C T T C A T G G C A G G A A T T C T C A T T C T G T T T C T A G G G T T G T G G C T G G C C A T C A G T T C A A C T A G C C C T G T C C C T G A T C C A G C A C A C A T T T C C G T A A C T A C C C T A G A A G T C A T G C A A A G A G A A A T G A T G A
WI-10810	58 C T	C A T C T T C A T G G G C A G G A A T T	A T G	G G A C C A A C A G A A T T A C T T G G C A T T C A G G G T T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A T A T T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G G C A T A T C T A A
WI-10828	23 T C			T A T G C C T T C C C A C G A G C C A T C C A C G T G C T C T T A G C A A A A A A T A G A A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C T C G C T T C T A A G T C A C C T G C A G T T A G G T C T G C A G A C A C T G T G T A T A C C A T A T A A T C T G A T T C T G A G C A G G A G G G A G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T T C G G
WI-10832	91 G C	C A T T A A T C T G C A G G C T C T C C	A	G A T T T G A G T A T T A C A A A T T G C C C A A A G A C C A T T A A C A G A T T T A A T A G T T A A A G C C A A A C T A T A A A G A A T T A A C T G T T C A A A A G T G T T A A T C T T A A T A C C A A T T T A T A G G C C A C C A T T A A C T T C T G A A G A A A G G T C A G C A T A T G C A A C T A A A T T T C T A A A G T C C A G T
WI-10834	96 C T	A G A A T T A A C T G T T C A A A A G T	T G G C C C T A T A A A A T T G G T A T T A	G G A T G A T G T T C T G T G G T C C C T T A T T C A A A G C C T C T T G C A T C C C A A A T G T G A A A T T A T T T A T T C T T G G T A T T T C G C T A C C C A T A G T C A C C T G T C A A G T G T C C A C C C T
WI-2287	24 T C			

WI-2296	81 A	GA	TGTTACTTTGA TTCCTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCTAGAAAGGCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCCTTGCTCTGACAGCCAGTTAGCTGTGTGATTGCAGAAAGTTACATTTGTTTGTG
WI-2300	77 GT	CCAGTCATAC	GGCACAGAAG	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTCGAAATTTCCCTTTATTGAGCGGGCAGGTGGTAGGCACAGAAAGC CAGTCATACGTTTGCCTTAAATTTGACCCCAACCATTAAGAAATAGCATTCA
WI-2371	55 GT	CCAGCTTCT	GTCTTGTTCTT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGCTGGTCTGTTCTTCCAGCTTCTGTTGTTGGTGGCT GTCAATCTTTGACATTCCTTGCTTGCAGCTGTATATTCATTCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTCTGTG
WI-2395	122 A	C TACTATCAA	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAATTTAGCTACAGTGCATATTAAGAGATAACATAGATATCATATAACTGGTTTAC TGAAATCTGAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAAAC/CJCTGAATTC AGAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTAATTAGTAACAATCTTTA CAATTACAAAAACCCA
WI-2437c	192 GA	---	---	---	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 GA	---	---	---	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 GA	---	---	---	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 GA	TTTATGTT	GCAACCTACT GACAAATTTAA	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATATGCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTACCTGCAGAACT
WI-1356	123 TC	GAAAAA	TGTTTAGGAA ATAATGACAA	TGGTTACAACCT GTACCAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTAAATACAAAACACAATGTAAATGCT ACATAAAATAATTGTCATATATTGTTTAGGAAATATGACAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C/A	GGGAGAAGA	CAGAGTCTGG	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGAGAAAG[C/A]AACGAGATAAAGCATG GCAAGAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGAGAAACAGAGGAGCGTT

WI-2906b	77 T A ---				CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATCTTCTGCTGGAACCTTGCCTGGAATGCTCTTCCCTCTT/A/GAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTCTGACCAACAAA
WI-2906a	50 A C TCTTCTGG	GACACCTTCAT	AGACCATTCOA	GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATCTTCTGCTGG/A/CJACTTTGCCTGGAATGCTCTTCCCTCTGAGCTTGGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTCTGACCAACAAA
WI-1736	175 C T ---				TACTCCTCATCTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTTCCACCCCCAGCACTATTTACACAGAAACAGCATGGAGCAGTTTGAGTCTGGCTCTTAGAGAAGCTTACTTAAGGACAGTGGTTTCCATCTGTCTTCCA/C/TJAGAGATCTAGGGTGTCTTTTGGAAACCACCTTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT	CACTAGCAATG	TTAAACTGAAG	AATACCCAGTCTTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGAGGACACAAACATTTAGACCATAGCATTGAATTAECTATAGATGTGTTAAGTAATTAATAACATGGTACA/GA/JACAACITTCAGTTAACATTGCTAGTGATTCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCC	CCCAAACAC	ATTGACTAAGA	CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTACGACCCCAACACAGAGACCCCG/A/JTGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTTCTCCCTT	CTTAAAGAGA	AAAGTCGAATT	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTCTTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTC	AAATTCAACC	ACAGATCTAT	TGTGATAGTTT	ACAACACAGCAAAATTCAACACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAAGAGCAAGGAGACATATTACTGTGAGGAAGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC	TCACTCAAACT	AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGAGGTAGGGAAGGTGGGCAACTTCCGCAGCAGAGAGGGAAGAAAGTTCAAGACCGTTGGTAGGATAAGTGGATCAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAGATAAAGA/GA/JCCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC	ATGACAATGAT	GTAAA	ACTCCACCACAGTTTTGTGAGCCCAACCCCTGCATGGTCTTTTCTCTG/C/JTTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA	GAGGACTTAAA	AAGGAGCATT	CTGCCCCTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCCTTACAT/GA/JCAAATGCTCTTTTTAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCATTCAGAA	ACGAGACAAA CTACCTCTAAG AG	TCTGGTCTCCTCCAAGTTGTAGCATTCAGAAGTC/CTCTTTAGAGGTAGTTGTGCTCGTCTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGTCTACCTCTGACGCCACAACATAATTAATCCCATTCCTTAAAGAACACAGG
WI-3453	70 C T	TTCTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAAACAAATTGAAATCAGCTACTCTTCTTAGGOCATCAGAG AATC/TGAAGTCATGGGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGTCACTGTTTGA GTCAGTTCCCTAATTTAGCAC/AGTGATTTTAAATGAGTGTGTGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3474a	90 A G A C	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGTCACTGTTTGA GTCAGTTCCCTAATTTAGCAC/AGTGATTTTAAATGAGTGTGTGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3502	79 C T	CGTGGTTTCT GGATGTCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTC/CTTGGAGACAGGGTCACCCAC
WI-3600b	146 G C A T C T	GGTTCTAACC TGGATATAAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGGATA TAAACATCTG/CTATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG/TGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTCTGTAA GAAAAGCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCTG/TCTTTTGG ATAGATGGTTGATAGGAGATGGGTGTTAAGACACAATTAACCTTGTGTTTTCAGGCAGAAATAG ACTCTCTGTGTAATCACTGAATGAGTCCAAAAGCCTTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/CJAAAAACTACTATAGTTTATGAAAAATGACTTCCAAAAATCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAACTACTCTCTGTCATCTTAACCTTGACTGCACAG
WI-3735	72 T C A A A C	CCTCAGTTATG TATCAAATGA	GGCTCACCAAT CATTTGTTTT	TCTAAATGTGAAACCAAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAAC/T/CJACACCGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGGCAATTAACTC



WI-1819	51	CT ---				GAAAAGCAGGAAGCCAGGAGGACAAAACCTTTTGA AAAAGTCTTTT CAGCAC[C/T]TCGTGGATCCG AATTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTTGACTTGTCCAAATTAATGAAATGTGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGAATACG
WI-3746	116	GA ---				GGCCTATTCACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/G]A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C CAA	ACAGTCATTT AGTCTTCTCTGA	TAAGATAACC ATACTAGGTAG ATCOG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCCCTTCTGCTATAG CATC
WI-3898	25	A C G	TGACCAATGTC TTTAGAAGCA	TCGTGGTGTG CTCTOC		CAATGACCAATGTCTTTAGAAGCAG[C/G]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT
WI-3901	114	A G ---				GGACCAATTGCTCCCTCAGAAAGTACATTCAAGCCCTGGAGGCTGTCTTACACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGTAACCTCGGCTTCTCCTCACCTGACAAGTG[C/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	CT GC	TGATCTTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAG[C/T]ACCATCCTTCACTGCTTCTAGACCTATACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A A	CCAAGAGGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCAGTCCCAGGCCAAGAGCGTCTCTATGAATCATG[A/C]ATTTGTTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTTGTGTCATTTTGTGCTTCTCTTATGTAACAAATCACCACACATTGAGG TCTTAGTCATTGCATG[A/T]GTATACAATAATGTCACTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G CAA CAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTCTAATAT AGCC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCTTTTGGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G AACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGCAGCAA ATCATGATG	ATGCCCTGGATATACITTTCCAAATGACTAGTATGAATAAGCAGGTATTAATTTACCTATTATATTT AT/C/CATCATGATTTGGCTGCTTCTTTCCAAATTTACTACAAATTTGATTGTGCATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4189	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA/C/CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACA TTCTGCTGTCACTGGTGGCTG/C/TGGTCTGCTCTTCAATGTTCAACTGCTTGTAT CTGTGCCACTAAGGTATCAGGTTATATGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
WI-5163	24 C T	CTGTCACCTGGT CTGCTGT	AGGAACAGAC C	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTTCCACCAAGTGCTAAAGCAGTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGGGTGGGAAGGATCTGTAAAGG/C/GTAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4250b	117 A G	---	---	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTTCCACCAAGTGCTAAAGCAGTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGG/C/TGGGAAGGATCTGTAAAGGATAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCTTCCAC	TAAATGTCTCGGGAGATAATAGAAAGGTCCCATCCCTCTGATACCTTGGTCTCCCCATCACCT G/C/CCTTACACAACITGAAGTAGGCCCATCCAAACACTGGTCAGAAAGATACTGTCTGAC ACAGCTCTTCAAATGGCACAAATCAAAGCACCAGTAAAGCAGAGGCAAAATCTGG/C/TCTCAC CAITGGAAAAGTCTTGAAGGATAAGGGAGTGAATGACTGCTAGAAAGAGATGATTGGCCTT AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGATGCTCTTCAAGATATCACAGCCAC GATG/C/TTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325b	71 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGATGATGGCAGGAC/C/TGGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	---	---	TGGCAGAAAGTGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCCTGTCACTTCT CTAGACTCTTGACCTTGAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCCACTCCAGCCAG GGCCCTGTATCTGTTACGGCC/C/GJGAATGCTACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-4347	158 A G	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGTTGTTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCAGGGGTACTTGTATCACQ/C/CCTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCCAGGAAAGACTCTTACTTCCACTTGAGAAAAGGAGGAGGAGAGA AAAGAGGACTTTGACACACAACTTGGGA
WI-1936	117 T C	---	---	---

WI-5204	54 CT	---	---	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTGGGTTTGAAGAA[C/T]GAAGAAAAA TGAAGGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTGGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 AG	CTCAAAA	TTGGC	TTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TATAGGCGGAAACTATCTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 TG	ATATAA	GTCTTT	CCCTGAAATGTGCTTTCCTCTCCCTCAACTCTCTAGGAACTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTTAATTAACCTGTATCAAAAGAGATGGGTATATAAT/GJAAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49 CT	TATAGTCC	GCATGA	ACACATTTCAATTTGCTTTAAGTTGAATTTATCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTGGGGCAATTGATTGAATTGT
WI-4461	49 AG	CCCTCC	ACCAATTTCA	CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCTCTCC[A/G]TGAAATTTGGTGAAA GGTCAAGAAATGAATCCCACTTTTAGATTTCTGGAATTTTATTTGGGATGATAATGCAATGGGC
WI-4465b	75 GA	---	---	CTACTGGATTTTACTTTGCTCAAGCCAGACAACAGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT TCACCTTTTG[A/T]ATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41 AG	ACACGAAAGT	TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACAGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACTTTTGTTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160 TC	TAATC	GACAAAA	GGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT/GJCAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCT/CJCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 TG	ATGCTCTGAGT	GCCTTG	GGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT/GJCAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 TC	AAGATG	AAAA	TGAGAGATTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTTTTATATCCTATGATTATTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTGGTGGCAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G C A T C C	GCACATGTGG	GACAAATGCAGC CATGCA	AGCTTTCCCTTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTACAGTACTTTGCAATAAGCACCATGTGGCATCCAGTGCATGGCTGCATTGTCCAGTC AAATGAGACAACTTCCCTAT
WI-4582	226 T C ---	---	---	AGCAAGCATCTGGCAAGCCTGGTGACCAGAACATTAAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTAAGGCCAGTTTAACTTATTCCTGTACACA AATACTTTATGGGACAGCATTTGTAATCAATCAATAATGACTCGGTTGGCTGTACAAGCAT AAACAGACGCTTGCAAAATATGGTT/CJCCCTCCTTGTAGAAACCATTTGAT
WI-1965	105 G C A G	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGGCAACACAAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAGG/CJAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATCCACACAGATGGGAGTCAATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T T T G	CACTGTTTCT ATTGACCGTAC	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGTACGTTGTAGACAACCCAGAAAAATTAACAGCCTAC CATTTTTCACGTGTTTCTATTGACCGTACTTG/CJTCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G C C T A C G T T G T T	AGTTGTGCTG CTACGTTGT	TTTTAATTTT TGGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGTACGTTGTAGACAACCCAGAAAAATTAACAGCCTAC TACCAATTTTCACTGTTTCTATTGACCGTACTGCTTTTGTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69 T A A G C A C T G T G A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGCTTGTGCTTGAAGCAGAAAGCACTGTGA CT/AJCATTATTAGGCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTTGTAAACATATGGCATGGG ACATATCTCTGAGCCCATCACTATTGACAAAGATTCTCTTTTAAACA
WI-5252	119 A C ---	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT/A/CJTACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGCTACT TGG	TGCAAAAAAGGAAAAATGATAACCAAGGACTGTTGTTCAAGCAATGCTAGAAAAATATGCCTA/A/GJC CAAGTAGACAACCTAAGCACCTAAGCAGCAATGAAGTTTCTCTTGTGATTAAGTCTCTATTCA ATTACCAATTTATCGGGTAATTAACACTGGAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77 C A G C A A G A G G	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGGCAAAATTAAGCATATGAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG/CJCTTTTCATCTGCCCTGGTGGGTTTTCAGTAACCTGCAACATGCTTTGGCTCC CGGATGAAAGATACCCCTTCTATGACTCAGCAATTCACCTCCTAGGTATGCACCTAAACATGGGTG GCAAAAT
WI-4649	50 C T T T C C G A A T G	GAGACCATTTCT TTCCGAATG	TGTACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAAAATTTCTTCTCCTCAGTGAGACCAATCTTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTCTACCTGAATTTGATTTTTTAA AAAATCCTCCCAATATG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCTCT	CTGAAGTGTTA AACTGGATTGG G	AACTGTGTGTATGTTGTTGTTGTTTCTGGAGAGTCAGTTACTCTCAGTATCAATAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCTAGAACACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACACTTTCAGTAACGTT
WI-4677	82	T	C	AA TCCAAAAGTG ATTAGGTGAA CTT	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTGTAACATACGTGACATTTGGAAAAATTTGCCAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT[C/A]AGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAATTTTCCCTGGCAATGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G	A	AACCCACAC TGCACATGG G	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTGCCCCAGTTAGATGACTGCTCTCCACCCAGCTAGAAAAAGATGGGAGATTTATTTTC TGCACTATGGAACACCCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTC TAAAGGTCAGTAAATCACTTTGATGTTGAGATTTTCAAGAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	CCTGTCTCATC GGGTGCTAGA ACTAATCCCTC A	GGTTGGAACCT CAAATTACCTA GAA	GACTACAGCCACAGACAGGCAATGTGTGGCTTGACAGGTTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAGTGGCTTTCAGTTTACTACAGACCTCATCATCTCTCTGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGTCTCATCT[C/T]CTAGGTAATTTGAGTTTCCAAACC TGTGG
WI-2033	183	T	C	A	CGTTCTOC	ATGTTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTCCAAGGTTATACAGGACCAGTGTGGAAATTT AGCATTCTGGGTTTGGCATCCATCAGGGTGTAGAACTAATCCCTCAIT[C/G]GAGAACGTTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCTCTCCACCAATTCCTCATCTCTACTCTGTGA[T/C] AGGCAGACTTATATGAAAAAGGGA
WI-2034	150	T	C	CCAAGGAC	CC	CCACGACTATGCTTCAGAGTCCCTGGTACTGACAGAGAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGGGTTTCAAGTGAAGAACGATGAATCTCTCATCTCTACAGAGCTGGACTTCACCA CAGTGCACCAAGGACT[C/G]GAGCTGCACCTCTATCTTTACCCCTTCCGACACCAAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	CT	TGTCCTTTAA GTGTGAAGT ATTAATTAG CA	ATTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAAGAACATTCCTCAATCACTCACCATTGCTCTGTTATTGCTCTTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTGATA[C/T]TGATGTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCCATTT TGCAITTCATTGGC
WI-4782	113	CT	GATCAGAAG ATACTAGAA AATGC	GAACCTCTTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTCTCTTCAGTCTTTATGCTTATTCTTAGGAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAAGATACTAGAAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTCCAGAACGATTAC
WI-4788	65	AG	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGACTCTTGGAACTTCAGTGCATAGAAATCATCTTGCCTAAGTCC[AG] JTGAAAAAAAATATGCCCCAAATTTAATTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	TC	TCCAGAGAC CACTTCATTC	ATTTCATAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCACCTTCATTC[C/T]TTTGGATTATGAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAGGTGAAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGTCAGTGACAGAGCCA
WI-4818b	121	GT	TGATAATGGG GOCCTGTT	CCTTCCITTTA TATGTATGCCA GA	TATAATGTTTGTTCATAGTGGCATAGACTAGGTTATGTCCACACATGAATAACAATCTTATATA ATAATTTATCAAGAAAGGAAATATACATATGCGGTGATAATGGGCCCTGTT[G/T]CTCTGGCATA CATATAAAAGGAAGGCTAA
WI-4818a	43	AG	TTGCCATAGAC TAGGTTATGTC GC	CATATGTATAT TTTCCITCTTG AATAAAT	TATAATGTTTGTTCATAGTGGCATAGACTAGGTTATGTCC[AG/C]CACAATGAATAACAATCTTAT ATAATAATTTATCAAGAAAGGAAATATACATATGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAAGGAAGGCTAA
WI-5317	139	TC	TTCCATTCTG GTAGCAGGT C	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTGTTGATTCCTTTGCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGTTAAT AATATAATATATGATGTTATATATACAATTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[C/G]GAGTCACTTCTCTTTCATCTATTCTAGGTTATTGAGCCCCGAGATCTACCCAGG
WI-4888	56	GA	GCAAGATATA AAGATTAAAG AAAGATAACA CA	CAATCCACTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAG[AG/AT]GAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCTT
WI-5328	44	AG	---	---	AACATTTTAAACCATGCTACATTTACAACACTGAAAGACAG[AG/AA]AAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACAGTGATCTGGAAGAG
WI-4897	93	AG	---	---	GCCTTTTGAGTTTAAAGTCTTTTGGTGTCTTTTTCCTCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[AG/G]ATAAACACATCTC
WI-5345	29	GA	---	---	CCCTGCTATAGGTCAGTTTAAAAATCC[AG/C]CTGCTATGTTGCTTTGTTGAAGCCACATCCACT GAGGTATATTCTGCTGCATTTTCTATATCACTCAGCTTTCAGATCCACTCCATCACTTGCAG

Accession	Position	Sequence	Accession	Position	Sequence
WI-5370	143 TCATAAAACAA	AATAAGATGG TACCTTAACCTA	CAAAGTTGGTA CAGAGAATTTTC	143 TCATAAAACAA	AAA
WI-9711b	423 TA	---	---	423 TA	---
WI-9711a	390 CA	---	---	390 CA	---
WI-9702c	345 GA	---	---	345 GA	---
WI-9702b	344 CT	---	---	344 CT	---
WI-9702a	179 CT	---	---	179 CT	---
TIGR- A003N21	49 CA	---	---	49 CA	---
TIGR- A004V30	203 CT	---	---	203 CT	---

TIGR- A004W22	232 C A ---			GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGGCAGTG CCGAGGAGGGGAGGACAGTGGGACAGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACCAGGTTCACACATCATGCACAGCGGGCTGTAGCTTGTAGTCCAGACAG GCCTGCCACATTTGGTCTGCCCGCCCTA/CATGTGAGATGTCTCTAAAA
TIGR- A005D24 b	138 C T ---			CATAGAAAGGAGCTTTGAGTATTGTACAGTTTGAATAATCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTACCTCTTGTTCATTCCACATCTTTATAGAGAAATATAAACCCCAATTT CTC/TTTTCAACCATTTAGTTGATTATCATCTGGAATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
TIGR- A005D24 a	123 A G ---			CATAGAAAGGAGCTTTGAGTATTGTACAGTTTGAATAATCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTACCTCTTGTTCATTCCACATCTTTATAGAGAAATATAAACCCCA TTCTCTTTCAACCATTTAGTTGATTATCATCTGGAATTTCACTCAAGATGCAGCTCCTAAGATTATT TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
U03735	74 C G ---			TGAGTCTGACACGAGTTCAGGAGGCGCAGTGGAGGGGCTGGGCCAGTGCACCTTCGGGGGOC GCATCC/GTJTAGTTTCCACTGCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTCTGTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAATGTTCTTTTAA
U39840b	42 T C ---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAAT/CACACAGCAAAACCAACACA CAACCAAAACCGTCAACAGCATATAAATCCAACTATTTTATTTCACTTTTTCATGACACAACC TTGCCCCAGTGCAAAAGACTGTACTTTATTGTTTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56 A C ---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAATCAACAGCAAAACAA/CACACACA CAACCAAAACCGTCAACAGCATATAAATCCAACTATTTTATTTCACTTTTTCATGACACAACC TTGCCCCAGTGCAAAAGACTGTACTTTATTGTTTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41 G A CCCC			GTGGCCATCGATCTGGACCGTCCCTGCCACCTTGCTCCCGG/ATGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACCAGAACTGTGTCTCATGGT
WI-7008	180 A G ---			TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTGAGAA AGCACCAGTTTCATGATAGGCGTTCAGGTTCATGTTGACTGATGACCAAGAGTCAACATTCAG TTTCCACCAAGCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG/AGJAGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGTCTCGAAAGCCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26 C T GGGAACT			GGTCCACGAATTTGCTGGGGAATCTC/TGTTTTTCTTAAAGACTTTTGGACATGGTTTGACTCC CGAACATCAACGAGCTCTCTGTTTTTCTGGGTGG



WI-7593	46 G A ---	---	---	TTTTGTTGCTCTGGACACCCTGCTCCAGGATGAAAGGAGAG(G)AATGAGATCAGTTTTGGA CACTTCTCTTGAATATAAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ---	---	---	AGTGCATCTTGGGGAAAGGCTCCAGTGTATCTGACAGTCTCTTATTTTCAGGTGGGACTCTT GATCCAGAGA(G)GACAAAGCTCCTCAGTGAGCTGGTGATATATCCAGACAGAACCCAAAGTCTCC TGACTCCTGGCTTCTATGCCCTCTATCTCTATCATAGATAACATCTCCACAGCCTCACTTCACTTCCAC CTATTCTCTGAAATATTCCTGAGAGAGAACAGAGATTTAGATAAGA
WI-7059	43 C G ---	AAGCACCCA GCCATC	GCTCCTGCTG GGTCA	GCAGAGAAGAACCATGCCAGGGGAGAGGACCCAGCCATC(G)TGACCCAGCGAGGAGCCAA CTATCCAAATATACCTGGTGAAATATACCAAATTTCTGCATCTCCAGAGGAAAAAAGAAATAAA GATGAATTTGCAACTCTTAAAAAAA
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	TCTACTTTCTG CCTTGGGT	AGCAGCCATCATGATCTGTTTTCCACCCTTCACTGAAAGACACCATTAT(G)TACCCCAAGG CAGAAAGTAGAACTTACTATTCAATAATGTTTGACACAAATTGGAATTGTC
WI-7079	293 T G ---	---	---	AAGGGCATTGAGACTATAAGAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACGTGCAT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTCTATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTTATACATTTATACATCACCTTTTGACTTTTCCAAAGCCC TTTACAGCTCTTGGCATTTTCTGCTAGGCTGTGAGGTAACCTGGAT
WI-9074	38 A G AAAAG	GGTAAAAGTT CTTTTGCTCT	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTGTCTAAAAGAA(G)AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAAATGTAACTGT
WI-7104b	249 C T ---	---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAAGAGAGAGTGCAGGAGACCTTGAGGCGAGCCGTTCTACTTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCTTGACCCAGGTGGGGCCACAGCACCAGCAGCATCTTG(C)TT
WI-7104	157 C A ---	---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAAGAGAGAGTGCAGGAGACCTTGAGGCGAGCCGTTCTACTTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGC(C)A/CAGCAAGAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCTTGACCCAGGTGGGGCCACAGCACCAGCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTCA(C)TGCCAGCTCAGCCCTACACAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CCTGGC	CCTAAGCATTG CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTAGGGTGAGTTAGCATTAACCCCAACCTCATTTTAGTTGCTAAGCATTTGCCCTGGC(C)TTTC CTGTCTAGTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	---	CCCTGTTCCCATGCTGACTGTGTTTCTCTCCAGTCATCTTCTGTTCCAGAGGTTGGGGCTGGAT GTCTCCATCTCTGCTCAACTTTAT(T)G/GTGCACTGAGCTGCAACTTCT

WI-9014b	44 C T ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCGAGTCATCTTTCTCTGTTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGCACTGAGCTGCAACTCT
WI-7023b	206 C A ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCTGCAGATCCTCATGGGTTTGTGACAGACACCTGCGTGCT CAGTGGCCCTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTCCCC TCCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCTGCAGATCCTCATGGGTTTGTGACAGACACCTGCGTG GCTCAGTGGCCCTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTCC CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	CTGAAATCCCTCTCTGCTGGCTGGATCCGGGACCCCTTTGGCTTCCCTCTGCTGGCTCCCAGCC CTACAGACTTGTGTGAGCTCAGCCAGTGTGCCGACTCTCTGGGCCCTCAGTTTCCCAGCTATG AAAACAGCTATCTCACAAAGTTGTGGAAGCAGAGAGAAAAGCTGGAGGAAGGCCGTGGGGCCAAAT GGGAGAGCTCTTGTTATTATTAATTGTTGCCGCTGTTGTTGTTGTTA
WI-9171	62 G A ---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAAGTAGAGATAATAATCA(G/A) TTCTTTACAACCCGATGGTAATTAAGCTTGTTATTCACAAGACTTCATGC
WI-9174	47 T C T	---	GTGTGAGACCATCATGGTGCCAGCTAGGACCCCATCTCCTATTTAT/C/CAGTCCTGTCTCTATATA CCCTCTAGAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52 A G	---	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAAGAACAGATAGATCCCTGTATT TCAAGACCTCTGTGCACCTATTTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAGTAAATGTTGGGTAGAA
WI-9186	76 G A	---	AAAGAACTACAGAGGACGATGTCCAAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA(G/A)ACCTAGTCAGACTTCCCTTTTCATCTT
WI-9193	94 G A C A	---	TTGGACAAACCTAGAAATTTCTCCCTTATGTATCTCTATCGATTGTGTAGCAATTTGACAGAGAATAA CTCAGAAATATTGCTGCCCTTAAAGCA(G/A)TACCCCTCCACACACACCCCTGTCCTC
WI-9015	48 C T ---	---	TTTGGATTGATATCGTGAATCCTCAGCCGAGAAATGGGCTGGATTG/C/TGCTTTGGTTAATACAT CTTTCCCTTAAAGAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	---	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGAGGCCAC(G)GTCCTTATGACACCCACTCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGAGCAGCCACTCTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32	G C	CAGTCCCA GATTGA	CAGTCCCA ACTCAGAC	GTGAOCTGTGAGGTCAGGTCCTCCCAAGATTGA/GC/GCTGTGAGTGGGCAAGTGTGTCAAAAGGGG TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTTGAGCCGAAGAAGTCA
WI-7836	120	T C C	CAATAAACA ATGCAACGTTG	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGAAATAGAGAGTTGAGATAAACACTCTCATTAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAATGTATCATGGTGGTCTATAAATCCAAATAAAGATGCAACGTTCC/TG/GATTCTTAAT CTTGTTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACAGCT
WI-7286	65	T C A	CAGCTTCAGCT TAACTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCTGCTCCCAAGATTTTCAGCTTCAGCTTAAGTACAGAT/C TGTTAAAGCTTTCTGTTAGATTGTTTTCATTTGGTGATCATGTCTTTCCATGTGTACCTGTAAATTT TTTCATCATATCTCAAGTAAAGTCA
WI-7858	91	T G TAAAT	CTAAGCATGT ACGTGAATTTT	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAATGTTAATAACAATATGAATTTTCTCATGCATACCTATTACTACT AAGCATGTACGTGAATTTTAAAT/GT/TATAGATGTAAACCTTTAATAAAAAATGGGGTGTGG
WI-7860	50	C G	A	---	GAAGATTAGGGAGGTTGCTCTGTGGTCTCTCCCTGCCCTCTCCCA/C/A/GTGGGAGAGACC TGTAATTTGCCAAGTCCCTGGACCTGGACAGCTACTGGGCTTATGGTTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGAGGAAATGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGCCAG ACCTAGGTGCTCTCTAGAGGAAACAGGGAGACCTGGGCTCTGTGGAT
WI-9084	29	A G TTC	CGTACCTCCAA ACATAATTGA	GCTTGAGTGA AGTCTGCGAGA	CAAGGGTACCTCCAAACATAATTGATTGTC/GT/ATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTAGGGAGGCTGGCTACTGCTCTCTGCACTCTGCTGCTTG
WI-7307	128	G T	---	---	CACACTTGCTGTTCTTCTGAGTGTGAGTCTGCGAGGTGAGGTGAGGTGGGTAGCCGGGTTCCACA GGCCCCAGCCTGGCAGGGTCTGGCCCCCAGGTAGCGGAGAGCAGTCCCTCCCTCAG/GT/AACT GGAGAGGGGACTCCAGGAATGGGGAATGTGACACCAACATCTGAAGCCAGCTTGACACCTCCAGT TTGCACAGGGATTGTCTGGGCTGAGGGCCCTGTGCCCCACCCCCGCC
WI-9274	25	C T G	GAAATGTGAC TTCACTTTGGT	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTTGGTG/C/TCAATGGACAGAAAAATTTCTACCTGTGCTACATAGAGAA GTTTGAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGAAA
WI-7313e	266	T C	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTGCAAGTCTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATCAGCCAGTGTATCCACCAGTTTTTGTATTGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256	C T	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTGCAAGTCTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATCAGCCAGTGTATCCACCAGTTTTTGTATTGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAAATGTATAGCGATGA

WI-9281	68	GA	---	---	ACTGTGGGAGACTGTGAGGATCCAGGATTTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/ATGTTAGTTGTCAGTCTGTGCTCTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A GCTC	---	CATTTATTTG AAAGCTATTCA GACA	TTCTGAAATATAACCAGCCATTGAGCTATTTAAACCTTGTAATTTTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTCGTGACAAATAAACATTAAATGCTAACACATTTTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAAATAAATGTGAATGGT
WI-9304	70	GA ACTGA	---	COCCACAGAAC TATTGTAAAC AA	TCACGTTGGTGCTTCTCAGATTCTGAGGAAATGCTTTGTATTGTATTAACAATGATCACCGACT GA[G/A]AATATTGTTTTACAATAGTTCTGTGGGCTGTTTTTTTGT
WI-7933b	314	CA	---	---	TTACAGAACTTGCCTGTGCCTGTGTCCTGTCCTGAGGGCGGAGGGTCTTTTCTTCTTCTTTCC TACCTACCCCTTTTCTTTGGCCAGGGCTCGTATCTACCTTTCTTTGTCCTGCTGGCTGGCTGCAC AGAGGATTGCCCTTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTTGCACAA AGTCTAAGGAGCCATGGCTGCCTGGCTGGGAGGAACCATAGCTCCCT
WI-7933	96	GC	---	---	TTACAGAACTTGCCTGTGCCTGTGTCCTGTCCTGAGGGCGGAGGGTCTTTTCTTCTTCTTTCC TACCTACCCCTTTTCTTTGGCCAGGGCTCGTATCTACCTTTCTTTGTCCTGCTGGCTGGCTGCAC CACAGAGGATTGCCCTTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTTGCAC CAAAGTCTAAGGAGCCATGGCTGCCTGGCTGGGAGGAACCATAGCT
WI-7374	182	T A	---	---	CCAGATGTGCCCCATCAGCTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTGAACCACTTTCTAGCTGCTTTGAAGAAATATTTGT/AJCAGAAACACACAAGGCTT GAT
WI-9343	78	CT CCTCTGCCA	---	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTGCTCTCTCTCTCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAAACGTAAGTTTCATTTGGGCAA
WI-7386b	104	T A	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGTAATGTAAACAATTGTTA/TAGTGTTTAGAAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACCTTTTGTATTAT GCTCTTA/A/GTGAATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79	T C TTGG	---	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGGT/CJATTCCTCTAATGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T C GTTCC	---	GGTCCAGAAGA GCTCCGCTGT GCTCCGCTGT	TGTCCTCTGTCCCATCTGCAGTGGACCCAGGCAACCCCTTTGAGGAGTGGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCC/TJCGGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTCTGGAGGGTGGTGAATAAAGGCATCTGTCT

WI-7424	131	T A A A A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGCAGAGAAAGTTAGAGAAAAAAGCCACCGAGGAAAGG AAAAAACATCGCCAAACCTAGAAACGTTTTTCATTCGTCATTCCAAAGAGAGAGAGGAAAGAAAA T/AJACAACCTTTCATTCCTTTTCACAGCTTCAATAAACATTCCTACATA
X86400	118	A C			TCCTGCAAGAAGTTCTCAAGCCTTTTGTATTTTGTGCAATAAAGTACAGCTTTCATAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAATTTTAAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTCAGAAATCTAAATTTATGTACCACCTCGTTTATTGTTTCATTCATCCA TCCTTTTCCCATGAATATTCA
WI-8053	242	T A			GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGTCCCATTAAGAGGACCTTTTAAATCAACCTAA TAAACTCTAATTCGTGACTTTTAAAGATCTAAGGTCATTTTAAATACATGCTGAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTAACTTATATAAT/AJITCAGAAG
WI-6190	165	G A			TACAAATGAATGCTTTTATTCGGTATGTCATCCACATTTACAGCATTTAGTGTCTGAAACAGCAAG TGGAAGAGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG/AJGAAGCAGCAGCAGCACCACCAAAACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACOCOA
WI-6275	148	G C			AACAGTCAACCAACCAACATGACAACCTGCCAGGCAAGCCTTCTTCCCTCCCTTTGCGTCCC ATGTCCCTAGTCAGCAAGGTCCGGGAGGCACCGATGTTAGCTTCCGCCAAAGGAGTATTACAGAGA GAGGCTTGGGAA/G/CJGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACCTGGTATGCTGAA
WI-6421	41	G T			ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGTG/JGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGACGAGGACGGAACCGTACCTGAGAGGGGATGGGGGCTCTCTCAGAAA GAATATTTGGGCGAGAACCTTGGAACTGGCCACAGGAGACATCCCAAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A			GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCGTTCACTTTTCTTCCACACACTATGTACAGTCAGTGTCCAA GGTGATGGGCTACAGTGTGTCATCAGTGAGTGTGTACACACATTTTACATAAATTACACACGACTC ATACATGAAAAA/T/AJAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAA
WI-9420	202	G A			AACTGTTTACAAAAAGGCTTTGCAAACTTCATTACTGAATTGTAAGTCAATGACTGTGTTGTTT TAAATATGTACCAAGGAAATACAAATTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACAGCAGGAGTGAAGGAAACCGGAAACCCATTGTGTACACTGTCTTCACACAG G/AJGCACTTCTTCTACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTACACTTCATTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGTAAACCTACATAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCOC TTTTAAGAAAATGGCTTGTTCCAAAGGTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGAATTTATCCAAAGCGCATGTTCTTAACGTGCGCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTCCCACTAATCCACA GATCTGAAAAAGTACAGCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCAACAGGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCCCTTCTTAAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTTAAATTTCAATTTATCATCTGGACAGCCCCCTTCTTAAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAGTGATAAGGACAGGTCTAGAACAAGCGTCCCAACCTGGCACCAATGACAGTTTGGACCAAA TAACCTCTTTGTTTCAGGGGACTGCTCTACACATTTGGGGATGTTAGCAGCTCCGCTGCTTACCCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCCAACAAATCATGACAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCCAATGGTGGGATTGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAAACCGTTGGCAAGGCTCCCCAAGACTCACCAACCCCACTTTGGTGTACCCCTATGCCGGGTG GGATTGAAGAAATAACCAATAATATATTGCTACAATTTTCCAGTAGTTACCAAGGCACCGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTGCTGGCTGGTCCAGGCATAGAGTT/G JGGCCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTTCCTTTTCTAAATGTTATGATTAATTTAGTGTCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]JAGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G ---				TGGTATTTTCCTTTCTCTAAATGTTATGATTAGTGTCTTTG/G/GAATTTGAAAAAATGT AAATCAGAGAACAGAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGAGCCCTGGGAAGAGGGATGAGAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGAAGCCCAAGGAAAGTTAAGT
WI-5896	61 C A ---				TTCTATTTAAATCTGTGCCCATTTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC/A/TAA AAGCCCTCAGACCCGAGGAGCAATGTTAGAACTAAATGACTGCAGGTGAGCAATCTCTGTATTA TACAACTGGGACCAAGAGATGACTTTATAATAGTGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T ---				TATTACTAGGTTATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCATTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGCAGGGAGCTGTGTCT/C/TGTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---				AGAAGACAGGAGACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTATACCTTCTCTTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTTCAGATGTGACTCTCTACATTCGAAACACTAGATGAGTAGGCTCTCTTCATCT CAATTGAAAATTTCTAGAA/G/A/AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---				TTTTGTTAAGCTTGTGAAGCCACACAGAAGTACTACTCTCTTTAC/C/TAAAGTGTACTTTTGA TATATTTATGGGATGATCTATCCCTACTTAAGATTTTCTCTCAGGTTAAATATCCATTTCCCT TTGTCAGGAGTTCTTATTGGCTTCTTCTAAACCCCTTAACCATTTCTGCTTATTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---				GAAACCTCGTTGGCTCAAAGGAAACTGTAG/A/C/AAATCTTTTTTTTTTTTTTTTTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCCTGCTCTTTTGTGTTGTTAAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---				AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAAGATAC/A/GJAGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGGCATGTGAGACCAAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTTGTCTGGTGTGCTGTGAGTCTGCCAGTCCCATAGTAGGTGTCCATAAATAAC AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179 C T ---				GATCTTTGCGACATGAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAAGTTAAAGTCTGACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAGGCTTGTCA/C/T/CTGTGCAAAACATTGAA AACAGCCAGTAGATGCCACTGATAGA

WI-1968	167	A G ---	---	---	TGGTGAAGAGCTGAAGGCTGAAAGATAGTCTCTGCTCTGGTCTTCGTTGGAATGGATGAGTCTCTTTACAAAATTTTCTCTGCGCATGGGTGTTATGTTAGATCATGGAGTTGGAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGT[G]GTAAGTTGAGCAAGTGTCTCTTAATGTCTCTCA
WI-4701	198	G A ---	---	---	GCCTCAATGCGCTTCCCTGTAA GGGTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAGAAAAATGGTGGCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCTCCCTCCCACTCTACCCGCCAAGTCTACCTTTGGTCTTTTATTCTGCTAATGACCATACTATTCCCAATTAGA[G/A]CCATGTCATTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---	---	---	TTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTACGTAATTTAAATCATGTCTCATTTAATTTGCACTTACTTGTGGTACCAGACATTGCTTCCAATTGTAAATCCCTAACACAGCAAGCATAACTGATGTCCATCTTTGTATTCCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGTCTTCTCTGTTTCACCTCTGTTTCCCTATTCCGATTCAGCATTCATGATTA
WI-4860	72	A G ---	---	---	AAAAAACAACCTTCAATTGACATTCTAAGAAGATAAGAAAAACAACGATCCACTGTGTGTTTGCCTTGATT[G]GGAGATAAAACCTGATCTCTAAGAAAATTAAACCAAGCAGTACACTAAAAATAGCCTTTGTGTGTGTTTTCAGGAAGAAAAGCCAATCCAAGTTGCTAAGAAAATAATGTTTCATATCACTCTAACTTCCACATAGAGCAATTAATATAGCA
WI-9705	111	C A ---	---	---	TGAAAGGACCAGTTCGAATGCTTACCAAGTAAAGTAAATCGGAGGGGAGGAAGTAGGAGTTGCTTCCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAAATTGTTAACACTGATGCTGTCTACAAACGACACATAGAAATCGGTGTAGATTGCGGTTCTAGTAAGTAGCTAATGTTTAGATA
TGR-A004Z48	177	A G ---	---	---	TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTGTAAGGGTGGGCGAGGGTGGACTGAAGATCTGTTGGCAGGCTCAGACAGACGCGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCATCTTGGGCAATACGGTTATCCCGTGTCTCATACGCCACAGA[G]TCTCCAAATTCAGGGGCTCCGTGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34	T G ---	---	---	GGGATTCATGTGTCTGTCTCATCCCAATAAGCACT[G]CATGACCTCAGCCCCATACTCTTTCTTCCC TATGTTCCAGAGACAGAAATAGACCTGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAGGACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTTCTAGTTGA
WI-7747b	88	T G ---	---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTCGTTAACTGTGTATGTACATA TATATAATTTTAAATTTGATT[G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCTTGTAAAGTT ATTTCTGTTTGTGTTTGGGTATCCTGCCAGTGTGTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTTTATGTTTGTGTTCTGA



WI-7747a	44	T C ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTGTATGATAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAGTT ATTTCTTTGTTGTTGGTATCCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAGTATATAATTTTTTATGTTTTGTTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCTCAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCATTATTTCCCTTCAACAATAATATTTTACAGAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATATTAAGCCTACAACATTTTTC/CJAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCGAGCTGGACTCATGGATGTCACCCCTTTGCTCCCTGCTCTTTCTGCCCTGG[G/A]CTCATGTA TCTGGCAGCTCTGTACCTCTGTGGGTGCCATCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAGGCACAGGCAAGGAGCCAGGACACAGAGCCTCAGCCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGGAATGGAATGAAATCAGGGGCTGCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTCTTCATCCCATCACCCCTAAATAGGTCAAGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[C/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTTATTTTAAAGAACATTGTTT GGTGGCAGCAATCTCCCTGCTCCCTATCACTGTTAGAGGCCCTAATTTATATCTATAAATATATAAA AGCAAGTCAAACTTGGATGATCAAGGTAAATATTGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTTCCGCGAGTCTTGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCT CAGGGGCTGGCACTCACCTTCTATTCTGTATGATGATTGTTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCCTAATCTGTTTAAATTTGTAACCTTTATTCATTTGAAAGTGTC AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAATTC/JACAACCTTT
WI-7928	101	T G ---	---	CTCCCTTCTCTATGCTCTCAGCAGCAGTGGGCGCACACTTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCATTC/JACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACTTTAAACCTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAITAAAAAATACGTACATTTGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTAATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTGGAGTTAAATGCACATATAGACATACACCCAAACACTTACACCAACIT/AJ ACTGAATGAAGAAGTATTTGGTAACCCAGGCCATTTTGGTGGGAATCCAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGTTCCAGCCGTTGCCCACTCATCTGCGCGCTTTGCTTTTGGTGGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGTC/JAGCCCAAAGTACAGCTGGACCCCTGGTGTG TGTAAGTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCATGGGCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	---	TTTCTAGGCTGTACAGTCTGATGATGTTTTTTTATAAATATTTTCACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGT[G]GTTAAAGGATCTCCACAATGTCGAGTGTG AAGGCAGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGCTAAACTGTGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCCAGGAGATTAGCAACAAGGATTCTCTGTACTTACTTGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTCTTGCCAGTGT [G]/TCTACTCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACCTCAAAAATTGGCAATGTCAATCAG
WI-140	252 C T ---	---	---	ATTGGAAGATTGGAGGGCTTTGCAGAGGAAAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTCTAAAGTGAAATGCAAGTTGTTACCAAGTAAAGTTTATA TCTCCATTGAGCCAGCTCATTGGCAGAAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCTTTGTCTGTATTGGCAATTCCTTC/
WI-198	218 C T ---	---	---	GAGGTCTTTAGCAACATGGAAAGCCCTACTGCTTCAACCCGAGTTCGCCGATCAAGTGTGGCAAC CATGATGAAACTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAAGCACTTCTCTTATCTTATCTCAGCTA CCTGCTTCCCTTTC/TGTTTAAACAAGCATAGATAATCTGAACAAC
WI-205c	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCTCATCTCTCACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT/CJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCTCATCTCTCACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT/CJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTCCAGGAGTTGCAGCCGTTTCTCTCGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCACCTGTTTGCACCCCAAGTCTTCCAGAGGTCTCAGACTACCTCTCCATCTCCCT CTCCCCACACACACAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGTGGGCTTTGAGC AATCATACAGAGTAATCTCTTGGTGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAACACATG/GCTTGACTCTCTTATCTCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCTGTGGCTGCTGCTGAACGGAGGAAAGATGGGGCGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTCTATCTCTGATGACTGGGCAAA

WI-276	25 A G ---	---	---	AGCTTTGAAATCCAAACACATAGCTTGACTCTTATCCTCCTTGTTGTAACATCTATCC CTGAGGAGAAATACAGAACACCCCTGGGCTGCTGACGAGGAAGGATGGGGCGGGAGACAT CGGTCAATGTATCAAAGCATCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGCTTATCCTCTTGCTATCCTGATGACTGGGCAA
WI-427	59 G A ---	---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAAATTTAGAACACTCTCC[G/A]GTTT TTTCCCTGGGAAATATTCACAAACATTTGGTGTGCTCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCAATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAITTTATAGAGCCAGGCTTGCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATACTTCTCCACTTCC
WI-562b	106 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATACTTCTCCACTTCC
WI-562	103 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATACTTCTCCACTTCC
WI-597c	141 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGATATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAAAC TTGATCTAATATTCTTCACAATAATATACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGATATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAAAC TTGATCTAATATTCTTCACAATAATATACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGATATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAAAC TTGATCTAATATTCTTCACAATAATATACCTGAGAGAAATAAGTCTATTAAAT

WI-611	66 G C ---			TTCAAAATTTAACACCATTGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCTTCTATTGTCTTGACGTATTACGTATTCGATCAGTCACCCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCTCCTACCTACTTGGGCTCTGACTTCTCTCTCTGGGCT GAACCTTCTCTGTGTGGCTGTCCGCTTCTCTGCTTGGGCTCCCAATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTCTATACCCAAAGTGTCTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTAA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCATTGTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTG/JTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGAGCAAGCACAATCTGTATGGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTCTATACCCAAAGTGTCTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTAA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCATTGTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTG/JTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGAGCAAGCACAATCTGTATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTGTG CAACCCCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCG/JATTTGTGTGTTGGC CAAATAATATCTCCCAAGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGTC AGTGCTATGTTTGAATGTGTCCCAAGCACAATCTGTATGGTTT
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTGTG CAACCCCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCG/JATTTGTGTGTTGGC CAAATAATATCTCCCAAGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGTC AGTGCTATGTTTGAATGTGTCCCAAGCACAATCTGTATGGTTT
WI-867	119 G A ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAACGTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTATTGTACATAA
WI-871b	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAACGTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTATTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAACGTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTATTGTACATAA

WI-884	198 T C ---	---	---	AGGTTCTGGACTTGATGCTGGGAAACAAATGGGTGCTGGGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTAGTGAAACATGATGAAATGAACATAAT
WI-921b	205 G A ---	---	---	CACITCCCAAGGCTCTGGGGGANGAGCGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 G A ---	---	---	CACITCCCAAGGCTCTGGGGGANGAGCGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTAAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTAAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	---	TTGCTTCAAGAAGTTCTTGCTCAGGAAGTTATTCAATTCAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	---	TTGCTTCAAGAAGTTCTTGCTCAGGAAGTTATTCAATTCAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	---	TCCCACTGAGTATGGCTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTTTATTGTTCTG CGAATTGTTGTTACTTTGGGAGAAATGCTCAACTATAAATGCTCTGACCCCTTTCTGTGTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 GA ---	---	TTGGCATTATTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAAACTTCTCCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTACCATAAATCACCTTGTAGGATGAACCTTATCTGGCCCAAACTGATA C[G/A]GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147 CT ---	---	GCATTGAGAGGGTTCGTTAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCTGAGTGTCTGAATCGCCAGGTGGC TAAGTCTGGGG[C/T]CTGGGGTCAGGCTGCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 CG ---	---	GCATTGAGAGGGTTCGTTAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 TC ---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTTAGACAGCCATTCTTTTGAATGN[C/G]GNCANT AAAAATGATTGAAATTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 CT ---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 CT ---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 TC ---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 CT ---	---	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNINNGCAATAATAATGGACAATCTTGNGNNNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTCTA/G/GC
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNINNGCAATAATAATGGACAATCTTGNGNNNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJCTTCTCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATTCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTTT CCTACCCCTCTAAATGTATCTTNTCTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATTCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTTT CCTACCCCTCTAAATGTATCTTNTCTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	GAGATGGCCAAAGACAAAGCAGAGGGGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCTTTGTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGATGGCCAAAGACAAAGCAGAGGGGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCTTTGTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAGTCTGTTATTTGTAAA ACACCAAGTGGCGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAGTCTGTTATTTGTAAA ACACCAAGTGGCGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAG/CJGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG

WI-1341b	136 G A ---	---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTTGTACTTTTGTGNTGCNNNTCCCTTTTCNNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNAATTAATACCCCAAGC [G]A]GGATTGTGATGGATCTGTTTATTTCTGTGCTTGGACACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCGAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192 G C ---	---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349d	264 C A ---	---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349c	192 G C ---	---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349b	264 C A ---	---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349	264 C A ---	---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1403b	57 C T ---	---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACGT AAAGTTTACATCAACATAATTCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGATCTGATTGT
WI-1403	58 T C ---	---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCT/C]TCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACG TAAAGTTTACATCAACATAATTCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGATCTGATTGT



WI-1417c	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTAGCCACCGGG GGTACAGCATGCCTGCTGGCATTGGAGGCCGCCAGGAATCCCAGTGGCCCTCTCAATGACTTG GGTCTCTGACTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGCGCGTTGC AGGCGAGGCCCTTAGGTCCTGATTAAATGTTTGTGTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTAGCCACCGGG GGTACAGCATGCCTGCTGGCATTGGAGGCCGCCAGGAATCCCAGTGGCCCTCTCAATGACTTG GGTCTCTGACTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGCGCGTTGC AGGCGAGGCCCTTAGGTCCTGATTAAATGTTTGTGTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTTCTACTCTGTGTGTATGTTAGGGGCGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTTCCGTTGGTACCTTCTCTCCACCACATCACCTGTGTTTTT
WI-1732b	122 T C ---	---	TGCCTTACTCTTTGTTCAATCCCAACCATACATTTTGTAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAAGGAGTNTCCCTGGGTCAACCTTTT/CJATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGTGATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	TGCCTTACTCTTTGTTCAATCCCAACCATACATTTTGTAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAAGGAGTNTCCCTGGGTCAACCTTTT/AACCTTTATTACGCT CTGCCACATGCTAGTAACTGTGAGTGATGGTGATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATCCTTTCCCAAAAAAGGTTTTTAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGTGGTAAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTACJA/GTJAGGCCCTTAACTTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTTCCCATCA ACTGGAGAGACCTTGTTGAGTACAGAGGACATTCAGGAATAATCATAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATJAGTAGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTACATATCTCTG GGTGTAAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATGAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTAATCTTGTGCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TJCTGTCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTCTGCTGTGGCT
WI-1837	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TJCTGTCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTCTGCTGTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TJGAGAACTCTGAATATTCAGACATACAAAGTGTGACAAACCCTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTCTCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	GGGCTCACCTTTCATCAGAGCACATATCAGTGATAGTGTCTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTAAGGACCTGCCNTTTTAC/C/TJGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCTACT
WI-1879b	110 C T ---	---	---	GGGCTCACCTTTCATCAGAGCACATATCAGTGATAGTGTCTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTAAGGACCTGCCNTTTTAC/C/TJGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCTACT
WI-1879	110 C T ---	---	---	TGTTCTCTGGTCAGGACCGGGCTAAGTCTTGTCTGCATAATGGAATATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG/C/TJGCTCTGAGAGGT AAAGTGCCTGCCCAACCGGCACAACTAGAGAGAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCATGAGAAACCCTTTCTTTGCTGC
WI-1900b	119 C T ---	---	---	

WI-1900	119 CT	---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCGATAATGGATAATCAACTGGACACCCCGNG CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCGAAAGAGGCTGCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCATGCCATGAGAAACCACTTTTCTTGCTCC
WI-1943c	165 CT	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACAGCCGCTGCTCTGAANCTGGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165 CT	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACAGCCGCTGCTCTGAANCTGGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164 CT	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACAGCCGCTGCTCTGAANCTGGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270 AT	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 AT	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 TC	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAGGAGTGCA TTCTGGGCATTTCTCATAGAGTNTTGTGTTTGTAGTCTCGTAATAACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTTT /CJTAAATCAACACTGGCTGAGGCTGTGG
WI-2012	102 TC	---	---	AAATTCAGAGCCAGAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCGCACAAACTAGCTAAAAATC/CJTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T ---	---	CTTTAGAGGTGGTCAATTCGGTCCCTCTCGGAAAGTGATTCTGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAACAGTCTCCAGCAGATAAATGCTGATACTGACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAAATGACTTTTGTTCAAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGGATATCTCAGCTTTCTGAGCCCTGTTACTGCAATCC
WI-2032c	166 G A ---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCAACCAACTGGTTTCTAGATGTACACG/GATGTGGGACCTCTGTCTCAACCTCCGACTTTTCAG AGATCATTGGTAGGCTCACCTTCTGTAAATTGCTTCTGTTTTCAAAAGG
WI-2032b	219 C G ---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCAACCAACTGGTTTCTAGATGTACACGTTGGGAACTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTCTGTAAATTGCTTCTGTTTTCAAAAGG
WI-2032	219 C G ---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCAACCAACTGGTTTCTAGATGTACACGTTGGGAACTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTCTGTAAATTGCTTCTGTTTTCAAAAGG
WI-2054b	188 C T ---	---	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGTTC/C/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2054	183 T C ---	---	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGTTC/C/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C ---	---	TGGGATTAACCCCTGTTTCTCTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTACAGCAGTAAATAAGCTCTTAAATGCACTTCCCGTTCACAAGGTGTTCCGTGCTTT/C/TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCTAGGTAAAGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTCAATATGGCTGGGCTTGGACGAG
WI-2573c	165 A/C ---	---	TGGGATTAACCCCTGTTTCTCTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTACAGCAGTAAATAAGCTCTTAAATGCACTTCCCGTTCACAAGGTGTTCCGTGCTTTTGTATAT CATCTGATCTTCCCAACCAGGGCTTATTT/C/TGCTAGGTAAAGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTCAATATGGCTGGGCTTGGACGAG

WI-2573d	129 TC ---	---	---	TGGGATTAACAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTT/CJTGGA TATCATCTGATCTCCCAACCAAGGCTTATTATGCTAGGTAAAGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 AC ---	---	---	TGGGATTAACAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTCCCAACCAAGGCTTATT/CJTGCTAGGTAAAGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165 AC ---	---	---	TGGGATTAACAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTCCCAACCAAGGCTTATT/CJTGCTAGGTAAAGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129 TC ---	---	---	TGGGATTAACAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTT/CJTGGA TATCATCTGATCTCCCAACCAAGGCTTATTATGCTAGGTAAAGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60 AG ---	---	---	GACTTCATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAGAACAAGCTTTCC/A/G/CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTTATAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 AG ---	---	---	GACTTCATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAGAACAAGCTTTCC/A/G/CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTTATAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 TC ---	---	---	CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGAAATAGAGCAAGGAATGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA/T/C/
WI-2870	131 TC ---	---	---	AGAAATGAATAGAGCCCCATTTAAATATATACAGCTTTATGTCCACTTCTGTTCCCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACATATCTGTTGTGGGACTTAAGTACAGACAAGGCATAAAAAA[7A]CAGCACCTGGGGCA CAGAGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACATATCTGTTGTGGGACTTAAGTACAGACAAGGC[7A]GATAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACATATCTGTTGTGGGACTTAAGTACAGACAAGGC[7A]GATAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA[7C]G CTGCCAGCACCAATAAGCTTCTTCAAAACAATTTGTGTAACCTCTCTCTTCAATAAACCTAAG ATTCTCTTGTCCCTGACATTCTGAAGCCACGCTGCTAGATGATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA[7C]G CTGCCAGCACCAATAAGCTTCTTCAAAACAATTTGTGTAACCTCTCTCTTCAATAAACCTAAG ATTCTCTTGTCCCTGACATTCTGAAGCCACGCTGCTAGATGATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTJA /TAAATCTTCTTCTGGT[7G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[7G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTJA /TAAATCTTCTTCTGGT[7G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 GC ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 AT ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995e	151 GC ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995b	151 GC ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995a	133 AT ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-3147	85 CT ---	---	GTGGTGAGTTTCATCTCTGGAGCTCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAAG ATCTCACTTAGCTCCTT[C/T]CTGCCATATCCTGTTTCTCTACTCTCTCTGAGACTTCTCTCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTTGCAAGG
WI-3234b	68 TC ---	---	ATTCTGTAATGTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGCCATTACCTCTACTTA T/C]GACAAGCAAGAACAAACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATCTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTNTATATCTTAT
WI-3234	68 TC ---	---	ATTCTGTAATGTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGCCATTACCTCTACTTA T/C]GACAAGCAAGAACAAACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATCTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTNTATATCTTAT

WI-3292b	106	GA	---	<p> GTTTTGCTAGACTAGGAGTTTCAGCTTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC  TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G]A/JTGGTATTGATTGGATGGGATGGATTACTT  GCCATGAATATTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAAAATATTATTNNCCATGA  GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAACCCATTTCATC </p>
WI-3292	106	GA	---	<p> GTTTTGCTAGACTAGGAGTTTCAGCTTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC  TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G]A/JTGGTATTGATTGGATGGGATGGATTACTT  GCCATGAATATTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAAAATATTATTNNCCATGA  GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAACCCATTTCATC </p>
WI-3355	19	GC	---	<p> CCATGAACCATGGGTACA[G]C/JATATTCCTAAACTTCAGAGTCCCTCTTACTGGAGAGGGATCCA  CTTTTAAAATATGATTTCTTGAAGTGGCTGCATACTATTCCCTCCAAAGCACTTAAACCTCATCAGAA  AAAAAATCATCAAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA  ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTNNAGTTG </p>
WI-3408	194	GA	---	<p> CCATGAAGAATGAGTTCTCCCTCCCTGGGTACGCTAAGAAATAGCACACCTTTGAGAAATTNACT  TAGCACGTGGCATTTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTTATGCTTTTCAAGCTTT  CTGGAATTGGGATGAATCTNACATTCATGTGCACCTTCTGTTGGGATCAGTTCTCC[G]A/JTGCCOC  ATCTCGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG </p>
WI-3505b	131	GA	---	<p> TAACCTATGCCTCATCTGGCTACTGCTTAGTCCCATTTGTGCATCAGTGCACCTTAAAAAATTATTT  GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTAACCTATTTTNAACCAAC[G]A/J  AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT  GTTTAAITGGGAAATATGTTTGCATAT </p>
WI-3505	131	GA	---	<p> TAACCTATGCCTCATCTGGCTACTGCTTAGTCCCATTTGTGCATCAGTGCACCTTAAAAAATTATTT  GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTAACCTATTTTNAACCAAC[G]A/J  AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT  GTTTAAITGGGAAATATGTTTGCATAT </p>
WI-3564b	177	CT	---	<p> GCTAGTAAGTTCCACCTAAATGGTTCGAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGT  GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG  TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGT[G]C/JAACAAGTGTTTGTGGTGTCTATC  AGTGTACACATGCTACCTTCCCTTCAAAAAACAAA </p>
WI-3564	177	CT	---	<p> GCTAGTAAGTTCCACCTAAATGGTTCGAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGT  GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG  TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGT[G]C/JAACAAGTGTTTGTGGTGTCTATC  AGTGTACACATGCTACCTTCCCTTCAAAAAACAAA </p>



WI-3649	64 A G ---	---	AATGTCCATGCTGTGACTGCTGTACACCTTTCCCTAGTATCCCTTAGTGAAGATTACAC[G
			AGACCAGTTTGCCTTCACTTAGTAGGGCCAAATGATAGACTTTTAGGTCTACCCACAAAGGGTACCTGC
			ACAGCCACATATATGTCACAGTATGGTTGCAAAAGGACCTGTCTAGACTCTTTCTGCCTGCCTTGGTC
			TTCTGTTTACCATAATTAATGATGACATGCAAACTCAGAGCCTTTTA
WI-3674b	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA
			ATTTAACTACAGGGGAGTCTTTTATAGTAATTTAAATATGTTTATTTAGAAAATACAAAATG
			/CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAATTTGTAACCTTGGTCAAAATGATTGTT
			AATCTTAATTAATTGTGTTTATGTTTNNATTAGTCCCAATCACAGCCCAAG
WI-3674	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA
			ATTTAACTACAGGGGAGTCTTTTATAGTAATTTAAATATGTTTATTTAGAAAATACAAAATG
			/CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAATTTGTAACCTTGGTCAAAATGATTGTT
			AATCTTAATTAATTGTGTTTATGTTTNNATTAGTCCCAATCACAGCCCAAG
WI-3682	137 G A ---	---	CAATATAGACCAAATGACTGCCACAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGTTTTT
			ATTGGCTCTCTCTCTCTCTCTTTTATGCTCTCTCCACACCAATTCACCTTATCTTTTCAA
			TG/AJAGCAITTTGCCAATTTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTAA
			GCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACCTGTGGTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGA
			CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCAGCTTAGGCTCTTGATTAACTC
			TGGTTCAGGAAGGCAAGGCAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAACG/AJAGAA
			GTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACCTGTGGTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGA
			CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCAGCTTAGGCTCTTGATTAACTC
			TGGTTCAGGAAGGCAAGGCAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAACG/AJAGAA
			GTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210 G A ---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTCTCATCTCTTATTTCTCTACTGCCTTCACTT
			CCATTACAAGAACTCTGTGATTACATTGTATGTTTGGTTACACTACAGAAATCCAAGATGACCTC
			CCCATCTCAAGGTCAACTAATTACACCTTAATCTATTTGCAATCTTTTGTCATTACCATACATATT
			CATGG/GAJTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130 T C ---	---	GAAAAATGATGTTTTTGTATTTCCCTTCTCTATCTTCAGATTATTGGAGTGTGATTAGAAAACTGATAGT
			AACCTTTTATTTGATGAACTCTGTCTATAATTAAACCTTCTCTCTCTCTTTATTTTGGCTT/CJACA
			GTTTAGGTAAATAAAGATGCCCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG
			GTAGGGACAAGTNCAGAAAAAGGAGGAGGTNGGGGGTTTTCTGGAAGA

WI-4110	130 TC ---	---	GAAAAATGATGTTTGGATTCCCTTCATCTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAAACTCTGTCTATAATTAAACCTTCCTCTTCCTGCTTATTTGCCJTCJACA GTTAGGTAATAAAGATGCCCAAGATTTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGNGGGGTTTCTGGGAAGA
WI-4119b	168 GA ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTGGGTGGGAAAGTAATAAATAG AATGGAAGGATAAATAAGGTAACTACGGGGAAGAACAGAGCAAGAACAGACAGAGAAGAGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTTGTATTAAGGGCTCTGTTGATCATCATCTCA
WI-4119	168 GA ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTGGGTGGGAAAGTAATAAATAG AATGGAAGGATAAATAAGGTAACTACGGGGAAGAACAGAGCAAGAACAGACAGAGAAGAGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTTGTATTAAGGGCTCTGTTGATCATCATCTCA
WI-4123b	51 TG ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATCTTCGTTACATAATTGTATAGAATTTAGTGGGG TTCTTCATGACATTTGGCTTTCTCTCAACAGTGGGTGGTTGGATGTTTCCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 TG ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATCTTCGTTACATAATTGTATAGAATTTAGTGGGG TTCTTCATGACATTTGGCTTTCTCTCAACAGTGGGTGGTTGGATGTTTCCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 GC ---	---	TTGTACATGTTTCATTCATCCCTCCCATTCCTTTCTGTCTTATAAAGAACCTCGCTTCCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGCCTGAACGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137 TC ---	---	TTGTACATGTTTCATTCATCCCTCCCATTCCTTTCTGTCTTATAAAGAACCTCGCTTCCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT T/CJGTGCTGTGCTTGTAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGCCTGAACGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188 GA ---	---	TAACACACTTTTCATTTGGTTTCTTACTGCAAGTTAAAGGACCATCCATTATATTAACAATTCCTC AGTTCTATGCTTTAGAGTNCATATAGGACTACTGTAAATTTTCAGAGGGAAATCTCTTGGAGTA GGGGAATGAGTTAAATATCTACCACATGCCAATTCAGGAGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCTTCCCAAGTTCTTAAATTCCTAG

WI-4230	93 T ---			AGAGACGTTGAATGGGGACATCTTTCTATTCGATTTTAGTTTAAACATTTGATAAGAAATTTGATGAAA GTTTGTACATTCAGATTTATCTTTATAGCAGCAGAAGCTGGCAAATAAATACAGCACACTGACT TTTCCATGGTAAAGAAGTTAGAGAAAACAGCCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTTAAATGGAGGAGAAATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 CT ---			GAAATTCATTTGAAGTTTGGACCTTGAACCTGATCTCATTAATACTTTTNCCTGTAGTGGTTGATTT CATTTTGGACACAGAACAGACGAAATTTCCACTTAAATTAATTTCTC C T AAGTATCTATGAT TTAGCACTGTTAGCACCCAGAACTGTGAATTAATCTCTAGATATCTCTCAGAAATCTAGGATGGAAG AA
WI-4271b	151 A ---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAGAGCCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCCCTTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAGAGCCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCCCTTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 GA ---			AATCGAAACATTTGATTTTGTAAAGGAACACATTTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAGATAGAAAGGATATTATTCATAACCTTTTGG AGGTAAGATGTGAACCTATACA G A TNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 GA ---			AATCGAAACATTTGATTTTGTAAAGGAACACATTTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAGATAGAAAGGATATTATTCATAACCTTTTGG AGGTAAGATGTGAACCTATACA G A TNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---			GATGACAAATTTATGTTGATTTGGCATTTTAAAJA G GTACCATTCATTTCTTCTGGCTTCGTGTT TGTTGTTGAGAAGTCAGGGTTAGTCGATTGCTCCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACTTAATACCCATGCCAAAGTACGTCCAACTGATCTTTAAAGAACATAAATCAAAATTCG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G O ---			ACCATCAATGTATCACCTTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAACCT GTCTTGGACATTTGAAATAAACAATTAATTTGTTGTTCTGCTACTTACAAAGGTACTGCACATA AACAAAGTTAAG G C G TTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACCTGTCA TTTCTTGTCCTCAATAAATAAATTTTACATGCTT

WI-4584	144 A G ---	---	TTGGTGGCATTAGCCTCATAACAACATATTACAATCATAAATGTTACTCTATTTTACAACAAG AAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCAAGATTGAACCCAGGAATCCATT CACCGGTACIAGTGTCTACCTGGGTAAAAATGTTTAAATAAAACTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAATAGGTGTGCTTAAATTTGTTATCAGTATGC
WI-4639	185 C T ---	---	TTCTGCATTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCAATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAATCCACCATTTAC TGACCATATGACTTGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATAATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	AAATGAATCCGCTTAGAGCAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA[A/- ]GATTACTATAAAGCATATTAAATTTATAAATATGGAAAAATTTAACTAGATAAATTAATGTGAAT TGAGTTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNGCT TCAATAGAATGGCTCTTTCGGATGACAAATGATGAACCTGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	GCCTTTGAGATGAAAGGGGAGCCTGGACCATTGCAGGGCTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTATTATTC/TGCTGTCTCCCTCTCTGGTATGCTTGTGTCATGAACAATGAATTG CCAGTGCCTGGCCGATTTCGTGGCTCCTAGAGGTGCCAGAAAAAAGTTTCGGTGAATAGAATTG ACGAATGGGTTCAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	CCCTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTATTTAATTT[G/A]AAAGAACTTGTTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5404	87 G A ---	---	CCCTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTATTTAATTT[G/A]AAAGAACTTGTTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5545b	77 A C ---	---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTTCTCACCACCTCACACTGCCGCA TATCTGCTC[AC]CCCAACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATATGGGACTATT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATTGAATTTTATTTTCATTCA
WI-5545	77 A C ---	---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTTCTCACCACCTCACACTGCCGCA TATCTGCTC[AC]CCCAACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATATGGGACTATT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATTGAATTTTATTTTCATTCA

WI-5860b	134 A G ---	---	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCITTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC/A GJTATACCTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCITTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC/A GJTATACCTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATCCCAACCCAGGTCTACTAACATTAACTAACCCCTAACCAATAC TATATTGTCCTGTTCTGAATTTATTTAGAACTCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAG TAATTC/GJATAGTAGTACCAACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTC/C AACCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAATAATTATCCCTGAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAATAATTATCCCTGAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAATAATTATCCCTGAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTC/C AAACCCTATATTNCTGTCCTGTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAATAATTATCCCTGAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTCAATGAT/CJGGATATCCCAAGTGCCTAGACAAATGCCTCCCATAC AGTGAACAGATTTTGACTAAACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCGAGG GAAC

WI-6244	103	T C ---	---	---	TAATTGCACAACCTACATATCAGGGTTCTGATTGAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATATTAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTAGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCAGGAGACATTTTATATCTCTACAGTGGGGGAGAGACTT CCTATTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	CT ---	---	---	CTGGCCTTATAATCCAAGTTTAGGATTATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTCTCTCTAGTAGGGCTTGGGTGTGGCACCCTTGGCTCATTCCTCTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	CT ---	---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCCG ATATATTCGCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAATGGACCATGTG GTACCCAGTGCATTATGTCCTGGTAGAGCCCTCTTGAGGACACTGACAGT
WI-6336	234	CT ---	---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCCG ATATATTCGCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAATGGACCATGTG GTACCCAGTGCATTATGTCCTGGTAGAGCCCTCTTGAGGACACTGACAGT
WI-6381	92	CA ---	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAGATTCAGATTTAGTTATGAGTATTTATACAATTA CAAAAATGNNTCATGTTTAAACAACAGTATTTAAAGCTCAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	CG ---	---	---	GGTTGAGGCATTGGGAAGGCAGAAATTTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAAGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAAGTTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGTAGCGTTTC GATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTTGT
WI-6449	186	CT ---	---	---	GAGGCCTTTTGCTTTCTCTCAGTCAAGGCTGATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGTCTCACACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTTCTATTCACTGTGCTCTGATCTTATGTCGGCTCTATTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAAGTTCTCTAAATTTCTGTGGTGTATTATA
WI-6449	186	CT ---	---	---	GAGGCCTTTTGCTTTCTCTCAGTCAAGGCTGATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGTCTCACACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTTCTATTCACTGTGCTCTGATCTTATGTCGGCTCTATTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAAGTTCTCTAAATTTCTGTGGTGTATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAGACCTCCAAAGAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACAT/CITGAAAAAAATTTAAAGTAGAACTCAAGAGCCAAAAGTCCCAATTTGTGCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCTCCTCCTC CAGTCCCATTTATATGACATTCGCGATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTAAATTAACCTTGGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGAGAAATCAGAGT/A/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTAAATTAACCTTGGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGAGAAATCAGAGT/A/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAAATGTTTNTAGGCCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TAGCAATATCTTA/G/ATCAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAATAATTGTGCAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTATGCG/A/CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATTTGAAGGCATTTGATTATNATTTTGTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6584	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTATGCG/A/CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATTTGAAGGCATTTGATTATNATTTTGTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

WI-6608b	46 C	---	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGAGGGGATTCCICCTAGTCCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6608	46 C	---	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGAGGGGATTCCICCTAGTCCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6666	68 C	A	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGCCCTCTCTNTCTCAAGTCCAGGCTTCTTGGGTAGACCACAAACTA ATACACAATGTTAGGCACACAAGAGA
WI-6670b	120 A	G	---	---	AGATTAAACATAATTACTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAGCACACAAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTTGIGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACACAGACACAGAAATCTTAGAAGGGAT
WI-6670	120 A	G	---	---	AGATTAAACATAATTACTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAGCACACAAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTTGIGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACACAGACACAGAAATCTTAGAAGGGAT
WI-6704c	33 T	C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T	C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAAC[T/C]AACATCATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T	C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAAC[T/C]AACATCATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG



WI-6710	106 G A ---	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTACAGCTGGAATGATCCCG(G)ATAGTAAACTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTATTACTGAGTCGACACAGGATGTCAACAGTGAGCCTC ATCTCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	---	AAACAAATGGTGCAATGCAATAATTGGGTCACAGTATAAACAATAACAATTAGTTTCATATAAC ATTGGATATGGACAAAATAACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN(G)CJAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAAC(T)ACCCAAATCCAGTTCCTCTTC
WI-6766	148 G C ---	---	---	AAACAAATGGTGCAATGCAATAATTGGGTCACAGTATAAACAATAACAATTAGTTTCATATAAC ATTGGATATGGACAAAATAACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN(G)CJAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAAC(T)ACCCAAATCCAGTTCCTCTTC
WI-6787b	97 A G ---	---	---	ACAGATAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAAATTCAC(G)JTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGTCTCTTGGGAAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	---	GAAACCAACAGGTCCTGTTATTTTATTAAAGGAGCATTTACATTTAGTAAAGTTCACACATTCAC TCAACAAGGCGGCTTCAAAATCAATCAGTCAACCCCG(C)GJGAGTTAGAAAGTAGAGTCATGAGGAA GAGTGTCTGGCTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C ---	---	---	CACAATAATAAAATCACTCCCTACCTGAAACCTTTAT(C)JAGAAAGCATTTTTTAAATTTACAACACA AAGCTCAACGACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGTAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	---	CACAATAATAAAATCACTCCCTACCTGAAACCTTTAT(C)JAGAAAGCATTTTTTAAATTTACAACACA AAGCTCAACGACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGTAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	---	GCATGATTAACCCAGTGCAGAAAATAACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAATCAACAATGTAGCT GCAGGGTAAC(C)A(J)GTGGATACCCCTGTGTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTCAGGTGGGCTGTGCAG

WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATAGCTAGCTTCTAGTA TTTGGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C]A]TGTGGATACCCGTGTGCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---	---	GATGGAAGGCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCCTAGTAAAGCCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTTCATATACAAAAATTTCTGCTATTTG CTTTAGCAAAACAGCAATAACTTTTGTGTTTCCCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---	---	GATGGAAGGCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCCTAGTAAAGCCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G]CATATACAAAAATTTCTGCTATT TTGCTTTAGCAAAACAGCAATAACTTTTGTGTTTCCCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAAGCTTTATTTGGCTCCAAACAAATATCCCTTTTAAACTCCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTTGAATTTTCAGATTTGCAGTTTATAGCAATTTTTCCTAAGAACCATATAAATAC ATGCAAAAACCTTGTACAT[A]G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTG TAAGCTGAATTTGCAAAATATGGAACACACACACTGGACTGGGTATACGTIG
WI-6826	154 A G ---	---	GCAAAAAGCTTTATTTGGCTCCAAACAAATATCCCTTTTAAACTCCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTTGAATTTTCAGATTTGCAGTTTATAGCAATTTTTCCTAAGAACCATATAAATAC ATGCAAAAACCTTGTACAT[A]G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTG TAAGCTGAATTTGCAAAATATGGAACACACACACTGGACTGGGTATACGTIG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTTGAACAAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACATAAGTAAATACAGCAGATGAGATGICICACATGAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTAGTCAACTTTTCAGTGTAAATTCACAAATATAGCAGCTCA AACACAAATGCAGGAGCAATGGCAAAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153 G A ---	---	TTATAGAATACTTATGGGGCATACGNGTAAATGAACGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCCTGAAATCCCTCCCTGCTCACAACAGCCAGCTACNGGTTTCTIAAAGACGTA ATTTTGCAGGCAAACTTC[G]A]TAGAGCCATTCGTGTCAGAGAAGGGAAGGAGGAGCTGTTTGT TTACCTGTAGTAGAAGATATCTTTGCGCTGTAGAACTGAGCTCATTAA
WI-6909	73 C T ---	---	ATTGAAAACTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAAATGAGAGAAGATGC AGACTTA[C]T]AAGCTTATAGAGAAAAGTCAAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATAATTTGCATGCCCTAGTTGCCCTATTTTATACATAIC

WI-6910b	163	GT ---	---	CACTCAAAACCTTTATTGATTTACAAACTGTACAATAATTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATAGTTGAGATGTAATGGAGAAATTAATGTGTAGAGAAA GTCAGAGTGGCTGACCAGTCCCGGACCTCCATGTGAATGACTCTCCCTTGGC GCTGTTTTTTTTGTTGTTTTTAAAGTGACACCTTGGCCTGTGGGCATTTCTTCACTTATCTTACCC AAAAGTGCCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGTAGTATTTTTCAGATTTCCACAAAAGACATG TATTGCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6915	144	A ---	---	CAATCAAAAAGTTCCAAAGTTCAAAGCTGGGATGAAAAGCCAGGCTCTCTGACTTGCACCTGTCTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTGTCTTGGTCCCTGTGAGGAAAGGGTCACTAAAGGTC/AACTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928b	175	T C ---	---	CAATCAAAAAGTTCCAAAGTTCAAAGCTGGGATGAAAAGCCAGGCTCTCTGACTTGCACCTGTCTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTGTCTTGGTCCCTGTGAGGAAAGGGTCACTAAAGGTC/AACTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C ---	---	TTTTATGAAACATTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC(G/A)NGTCATGTCCCAATCCCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATTAAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955b	79	GA ---	---	TTTTATGAAACATTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC(G/A)NGTCATGTCCCAATCCCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATTAAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	GA ---	---	AAAACTAAAAACCCCTTATTGTCTCCAAAGTGTGGCAAAAATAGAAAAAT(G/TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAAGCATTCAGTCAAAATATCACAAAA ACAAAATTCAGATTGCTTGGATCTTGGTCAATTTATGGCTTGAAGAACTGGATTGAAAAACCACTTTAGG CTAAAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6957	47	C G ---	---	ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCTCTGGTCGCCGCACTTCTGTATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGTCTTCAGACCCAGGAGGAGGAGCGCGGAGTTCCTG CAGGAGAGAGGAGGGCTGTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTGCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTTCTCTTCG/GTGTGCGGATC
WI-6996c	242	GT ---	---	

WI-6996b	242	T	---	---	ACTTCTAGTGCCTCTGTACCAACACCTCTAATGCCCTCTGGTGCCTGACTTCTGATGTCCTGAGCCTTAAATCTGCCTGGCGTCCCTCCCTCTGCTTCAGCAACAGAGGAGAGAGCGGCGAGTTCCTCTG CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTTCCTGCTGTCGGATC
WI-6996	228	T	G	---	ACTTCTAGTGCCTCTGTACCAACACCTCTAATGCCCTCTGGTGCCTGACTTCTGATGTCCTGAGCCTTAAATCTGCCTGGCGTCCCTCCCTCTGCTTCAGCAACAGAGGAGAGCGGCGAGTTCCTCTG CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTTCCTGCTGTCGGTCCGATC
WI-7021b	112	G	A	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCTGAGCTCCCTGTCTG CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAATGGAJCCGACTGCACCTTCTGTGCTCAGCTCTTGTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A	G	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCTGAGCTCCCTGTCTG CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAATGGAJCCGACTGCACCTTCTGTGCTCAGCTCTTGTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C	T	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGGCCCTGCAGCCTCTCCACCTC ACCTCCATGACAGCGCTAAACGTTGGTGAJCTGGTGGGAGCCTCTGGGGCTGTTGAAGTCACTTGTGTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTGATA
WI-7056b	118	C	T	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGGCCCTGCAGCCTCTCCACCTC ACCTCCATGACAGCGCTAAACGTTGGTGAJCTGGTGGGAGCCTCTGGGGCTGTTGAAGTCACTTGTGTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTGATA
WI-7091b	153	A	C	---	AATTGCTGAAAAAGGAACCTACCTATCCTTACATTCACCTACTAATGCTCTTCAACATCTTAGAGGTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATTCATCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTAACATAATTATTCATTGGTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A	C	---	AATTGCTGAAAAAGGAACCTACCTATCCTTACATTCACCTACTAATGCTCTTCAACATCTTAGAGGTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATTCATCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTAACATAATTATTCATTGGTCTTTTATCTGTTCTATATGAATGCTAT



WI-7175	194	C T ---	---	CTCTAGACTAGTGCCTTACCTTTATTAAATGAACGTGTGACAGGAAGCCCAAGGCAGTGTTCTCTACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGTTTACTGCTGCTCATTTGCCATGCCTA[C/T]AGAT AAATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACATGGG
WI-7178b	273	G A ---	---	TGTATCAGGTGAGGACCTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCGCTGCTGGAG AGGGCTCGCTGCTGCTGCTGCTGCTAGGGGAACAGACCAGTACCCAGAAAAGCATACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273	G A ---	---	TGTATCAGGTGAGGACCTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCGCTGCTGGAG AGGGCTCGCTGCTGCTGCTGCTGCTAGGGGAACAGACCAGTACCCAGAAAAGCATACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116	A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCACTCTGAGCC[C/A]CTCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGCTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTGGTAGCAAGATGGCAGCTATTTCCTGAAGCCCTAGTACCCCAAT
WI-7182	106	C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCC[C/A]CTCTGAGCCCTATCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGCTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTGGTAGCAAGATGGCAGCTATTTCCTGAAGCCCTAGTACCCCAAT
WI-7191b	273	T A ---	---	ATAATTGCTTGTTTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACCACAGCCACATCTAAGCATTTAGTGATGGTAGC TGATGTCAGCTTCATGTGGAATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAAATGTGTACCTATTAAATTTGTAACCTAGCAAGTAGAAGACCATTT
WI-7199c	112	T C ---	---	CCCAGTGGTGAACAGAACCCTCCCAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCCTTGAGGTACCCACCGTCTGTGAGCTCTTGAACCTATGAGCT[C/G]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTCTGAATTTCTCTTTATTAT AGTCCTATAGTTTACTCCTCAGTTCCCTACCATCATCATCTTGTCTAA
WI-7199b	112	T C ---	---	CCCAGTGGTGAACAGAACCCTCCCAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCCTTGAGGTACCCACCGTCTGTGAGCTCTTGAACCTATGAGCT[C/G]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTCTGAATTTCTCTTTATTAT AGTCCTATAGTTTACTCCTCAGTTCCCTACCATCATCATCTTGTCTAA

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WI-7252a	520 T C ---			CCACGAGATCCAGCCAAAGGGGCCCTCCCGCCCCCTCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCGGGGCGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCGG GACACTCCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCGAGGTGGAACCTCAGTCACTAGACTCTCTCTCCA AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265m	252 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265l	231 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265k	121 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265j	174 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265i	227 T C ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265h	80 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265g	170 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT

WI-7265f	231	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCAATTCGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGATTTTGTATATTAATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTT/AAGGAGTAAAGATTTGCCT
WI-7265e	227	T C ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCAATTCGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGATTTTGTATATTAATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTT/CCTTAAGGAGTAAAGATTTGCCT
WI-7265d	174	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCAATTCGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265c	170	T G ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCAATTCGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATAGTGATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265b	121	T G ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCAATTCGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATAGTGATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265a	80	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCAATTCGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATAGTGATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7281b	183	C ---	---	GATCACCCAGCCACAGCCCTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCAATGAAGCATCTCAGACTCTCTGGCAAAAACGAGTCCGCGAGGCCGCGAG GTGTTGTGAAGACCACTCGTCTGTGTTGGGTCCTGCAAGAGCCCTCTC
WI-7281	171	C A ---	---	GATCACCCAGCCACAGCCCTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCAATGAAGCATCTCAGACTCTC/AJTTGGCAAAAACGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGTTGGGTCCTGCAAGAGCCCT

WI-7282b	159	G C ---	---	TGTCACCTGGCACATTTCATTTCTCAGTTGAAGAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCACCTCAAAAATATGTCAACTTNNNNNNNNNT AGGCCCTTTCATAAAACCAAACTG/CJTAGCAAGATGCAAAATGCATGGCAAAATCTGTGGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATTAATCTCCCCACTCCACTAC TCTCTCCCTCCACTTCATTTTCC/CJTGTGCTTCTCTCTAATTCAGTGTGGAGGCCCTGACTTG GGGACAAACGTAATTATGATATATTGCTGTCTTCTCTCCCAATAGAAGAAATAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/JTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/JTGGGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205 A C ---			AACTATGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGGGTGGAGGATATGATGTTACATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGTGGGAACATAATGATTTGGAAATTACAGTGGACAACAGCAATCA AATTACITGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49 G A ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAAACCTTGTTTTT
WI-7314b	49 G A ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAAACCTTGTTTTT
WI-7314	36 A G ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAAACCTTGTTTTT
WI-7321b	199 C T ---			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGTCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGTCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---			AGACATTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGGCCTGGC TCCAGTGAAGTGGGCACATGCTCAGGCTACTATAGGTCCAGAAAGTCTTATGTTAAGCCTGGCAG GCAGGTGTTTATTAAATCTGAATTTGGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAATCTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[AC]CA
WI-7338c	221 A G ---			CTCTTTCTCAGCACATGATGGGCAACTAGAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTGCTTTACCTTGAGC CATTTATTGTGTCAGAGAAACAAAAGAAACAGAAATCAATATATAAATCAAGACTATCTGCAGCTA GTGTGTTCTTCTTTACACAG[A/G]TATACACACAGACATCAGAAAATTCGTGT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAAATATGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATAAAATTCAAAGACTATCTGCGAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGTGT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAAATATGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATAAAATTCAAAGACTATCTGCGAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGTGT
WI-7338	221 A G ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAAATATGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATAAAATTCAAAGACTATCTGCGAGCTA GTGTGTTCTCTTTACACAC[A/G]TATACACAGACATCAGAAAATTCGTGT
WI-7384c	146 T A ---	---	CCTATGCTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAAATACCAATTAATACATTTGATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTTTAACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACCTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGCTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAAATACCAATTAATACATTTGATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTTTAACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACCTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	CCTATGCTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAAATACCAATTAATACATTTGATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTTTAACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACCTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTTATTTTACTTTGCCCCCTCCACATTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTTGTTTGA CTTGCTGCTGCCAAGAACCTTTTCCCCCAAAGATGTGATAGTTATGG
WI-7388b	106 A T ---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTTATTTTACTTTGCCCCCTCCACATTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTTGTTTGA CTTGCTGCTGCCAAGAACCTTTTCCCCCAAAGATGTGATAGTTATGG

WI-7388	94	T A ---	---	TGAATCCTGGGTCCTGGCCCTGCTGCTAGCTGGTTATTTTACITTTGCCCTCCCCACCTTTT TGAGATCCATCCTTTATCAAGAAGT/AJCTGAAGCGACTATAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTTGCCACAAGCGTCTCGGATTGIGTTGA CTTGIGCTGTCCAAAGAACTTTCCCCCAAGATGIGTATAGTTATTGG
WI-7438	64	A G ---	---	TTAGATTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAAACCCTATTGGAACCAAGTCTCAGATTGNCATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAAACATAGTTTGNCCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACITTTACCA
WI-7454b	152	T C ---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAGCCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C ---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAGCCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C ---	---	AATTTGAAAAATCTGAAAAAAGTGCTAATAGCAGAGAAATGACACTTATTCCAAATAAAATTTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAACGTTCAACCAAAATTAT
WI-7464b	168	C A ---	---	AATTTGAAAAATCTGAAAAAAGTGCTAATAGCAGAGAAATGACACTTATTCCAAATAAAATTTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAACGTTCAACCAAAATTAT
WI-7464a	103	C A ---	---	AATTTGAAAAATCTGAAAAAAGTGCTAATAGCAGAGAAATGACACTTATTCCAAATAAAATTTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTAATTTCCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAACGTTCAACCAAAATTAT
WI-7499b	134	T G ---	---	CAATTCATCAATCCAACCTAGTCTGNTGCTTAAACCATTCAGACAAAACCTCCACTTCGAAGGTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCGACATCACGTTCTTTGAATGCTTCAIT /GJTATAGTCCCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGA ACTCTGTACAAAATTCCTTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---	---	---	CAATTCTCAATCCAACCTAGTCTGINTGCCCTAA[A/G]CCATTCCAGACAAACTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAGGAAAAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAGGAAAAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTTCGCAGTGCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGAACACATCCCGGTGATAGAATTGCT AAATTGTC/TG/GTGAATAGGTAGAAATTTTCTTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTTCGCAGTGCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGAACACATCCCGGTGATAGAATTGCT /CJAAATTTGTCGTGAATAGGTAGAAATTTTCTTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAAGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTTGAAC TAGATTGCATGCTTCCCTCTTGTCTT[G/A]GGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCCCTCIGGCICCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAAGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTTGAAC TAGATTGCATGCTTCCCTCTTGTCTT[G/A]GGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCCCTCIGGCICCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGTT/CJTCTA AAAAAGAAAGTGGTATGTTGTGATGATCAGCAGCTAAGTCTCGATTCTGTTAAAGCCACTTGGGTG ATAAGAAAGGGAAGTAAAAATGAAGTCTGACTAGAAAATTCATTGTCAGAGGCCAAGTACATTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGTGATGTGCAATTTTGAATTTTCAG

[illegible]



WI-7576b	168	A T ---	---		AATGATGATGATGATGACGACGACAAACGATGATGCTTGTAACAAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAAGTTTGTGT TCTGTTGTTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCCTTATTCTACATTTTCACCTAC TTTGTAAGTGAGAGAGACAAAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577q	77	T C ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	G C ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157	G A ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTACAC[G/A]TAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48	A G ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	G A ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T C ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	C A ---	---		AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTA[C/A]ACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117	A G ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTA[G]ACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77	T C ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50	G C ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157	G A ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACAC[G]ATAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48	A G ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G A ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T C ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C A ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTA[C]ACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117	A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAATCGTCTCATTAAGTTCTCTGAGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAATCGTCTCATTAAGTTCTCTGAGTA/GJTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619q	106	C G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGCGAGGAAGAAATGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCCATCTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCCATCTTTTCCCTC CGCTTCTTCTTACACAGAAACATTA/GJACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCCATCTTTTCCCTC CGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGCAAGGAAGATGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCGCGCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	ACAAAGCGGACATTGAAGAGGACGACGAGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAAGCGGACATTGAAGAGGACGACGAGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAAGCGGACATTGAAGAGGACGACGAGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATTGGGATCTGTCTGGC[A/G]TTAAACACATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATTGGGATCTGTCTGGCATTAAACACATCATGGACCAAAATGTG TACTAATGATGAGCAATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATTGGGATCTGTCTGGCATTAAACACATCATGGACCAAAATGTG TACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626	144 T C ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATTGGGATCTGTCTGGCATTAAACACATCATGGACCAAAATGTG TACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	TCCCATACCGCTGATCTCAGGGTCTGTGCTGCCGCCACCCAGATGGGGAAAGCAGCAGGTGGGC TTCCAGTGGCTGTGCCAGGCCAGACCTTCTAGGAGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGAGCTGTATACAAATTGCAGACTGTGTAAAAAGAGAGCCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAAATTTTCATATGAC

WI-7689b	134	A G ---				TCCATAACCGCTGATCTCAGGGTCTCTGCTGCGGCCACCAGATGGGGAAAGCACAGGTGGGC TCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCAGCAAAGGTTGTTCTCTAAQA /GTAAGGCAGAGTCACACTGGGGCAGCTGATACAAATGACAGCTGTGTAAAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---				TCCATAACCGCTGATCTCAGGGTCTCTGCTGCGGCCACCAGATGGGGAAAGCACAGGTGGGC TCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCAGCAAAGGTTGTTCTCTAA AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAATGACAGCTGTGTAAAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---				TGGAGAACATTCATCTTGCCTGCTACTTTCATCAATGAAGATTAG/AJCACTGAGATCCAGAGGG CTGGATGACTTGTCTCAAGTTCAACAGCATGGTAGTGGCAAAGAGAGGTCCAGAGTCTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATAGGGCCACCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACGTGCTGATCC
WI-7703b	164	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAAGTAAATGGTCTCTCACTGTTTATTAACTCTAAATTCCT TTCAATTTAGGGTAGCAATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAAGTAAATGGTCTCTCACTGTTTATTAACTCTAAATTCCT TTCAATTTAGGGTAGCAATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---				TAAATGAGTGTGTTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGGCCACAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---				TAAATGAGTGTGTTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGGCCACAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743e	106	C A ---				TAAATGAGTGTGTTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGGCCACAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCC

WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743c	106 C A ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743b	275 C T ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106 C A ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	275 C T ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	275 C T ---			TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCAGCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7758	144 A G ---			TGACATTTATTCAAAGTTAAAGCAACACACTACAGAAATTAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAAAGTGCATTAATAATTTTAAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGTAATTTGTTTATATTTTCCCATTTTGGAGTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCCTTGGCAGGTGCAGCCCCCAGCTGCTTTGACCTGCCCTTCATGCATGGAATTCOCCT TCATCTGGAACCATCAGAAACACCCCTCACACTGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGG GAAACATTCATCCTTGAGTCAAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAAACCAATCAGTGAACCTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGTATCAGATTATTTTAAGTTTATCCGTTAGTTT GATAAAGATTTCCTATTCCTTGTTCTGTGTCAGAGAACCTAAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTTCATGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCAGCTCCAGTAGCGAGAGACGGCACCCAGAAT CAGATCCAGCTTCGGCATTGTATCAGACCAACAGTGTGTTCCCGGGGAGGAAACACTTTTAA TTACCCCTTTGCAGGCACCACTTTAATCTGTTT[C/A]TACCTTGCTTATTAATGAGCGACTTAAA A'GATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAATGIGCTTGCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTATTGTCTGTAATACTGTAAATGCATTGGAATAAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCA TAATTTATTGTCCATTGATGATTTATTGTTGTAATGTATCTTGGTGTGC
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTATTGTCTGTAATACTGTAAATGCATTGGAATAAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCA TAATTTATTGTCCATTGATGATTTATTGTTGTAATGTATCTTGGTGTGC
WI-7785	156	T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTATTGTCTGTAATACTGTAAATGCATTGGAATAAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANN- /JNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCATAATTTATTTTGTCCATTGA TGATTTATTGTTGTAATGTATCTTGGTG
WI-7789c	84	G A ---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGGCCACCATCTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT
WI-7789b	84	G A ---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGGCCACCATCTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT



WI-7789	73 GA ---	---	TGTCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGGACCACATCTTACAGAGACTCTCCC TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAAGCATTTGACACACAGATGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACTCTTCAAAACCTTACAGTCCCTCCTAAGGTACTCTTCAIGAGATTCAATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCCTATGTCTTATGTGACTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/TT]TCTATACCTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACTCTTCAAAACCTTACAGTCCCTCCTAAGGTACTCTTCAIGAGATTCAATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCCTATGTCTTATGTGACTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/TT]TCTATACCTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTTCTCT TAATAAGCCCCACATATAAATGTACTTTTCTTCCAGAAAAATCTCCTTGAGGAAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATTTCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTTCTCT TAATAAGCCCCACATATAAATGTACTTTTCTTCCAGAAAAATCTCCTTGAGGAAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATTTCTG
WI-7814c	41 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGIGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATAATGGGATTTTC TTTTCTTTCTCTGTTAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGIGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATAATGGGATTTTC TTTTCTTTCTCTGTTAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]CATGCCAGTCCCGTTTCAATTTAGTCATGIGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATAATGGGATTTTC TTTTCTTTCTCTGTTAATTTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTCGCAATTTGATAAAATTAATTTGTTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTTGGCGIGGGA
WI-7830c	54	G A	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACATTTCTATGCCAAACAGGAAC ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTTGGCGIGGGA
WI-7830b	134	G A	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTTGGCGIGGGA
WI-7830	44	A G	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTTTCCCTTG AGGTTGATCGTTGTTGTTTGTGTCGCACTTTTACTTTTTTGGCGIGGGA
WI-7865e	25	C T	---		CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGCGAGGCAATTCAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	---		CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGCGAGGCAATTCAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	---		CCACTTCCTATCTGATTTTCCAGCAATGAGCGAGGCAATTCAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	---		CCACTTCCTATCTGATTTTCCAGCAATGAGCGAGGCAATTCAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/TAATGAGGCGAGGCAATTC TAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTTCAGGGTGCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGCGAGGCAATTC TAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTCAGGGTGCTTCCAACTGAAATCTCAATGTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	---	TTCAACACCTGCTTCACCCCTCCACCATCTGTGCAATCACCTTCAGCCTCAGCCTCAGTAGTCCCC CTAAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGC CTGTTGAGTTTAATGTTAATGTTGATTTCTTTAAGTAACCAATTCCTGTTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	---	TTCAACACCTGCTTCACCCCTCCACCATCTGTGCAATCACCTTCAGCCTCAGCCTCAGTAGTCCCC CTAAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGC CTGTTGAGTTTAATGTTAATGTTGATTTCTTTAAGTAACCAATTCCTGTTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	---	TTGATCGATCTTTCCACCCCTGTCACCTCAAGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAAATTTCCCTGCTTACCCCTATTCAGGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATCTAATGCGCTAGAT
WI-7868b	173 C T ---	---	---	TTGATCGATCTTTCCACCCCTGTCACCTCAAGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAAATTTCCCTGCTTACCCCTATTCAGGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATCTAATGCGCTAGAT
WI-7868	66 T C ---	---	---	TTGATCGATCTTTCCACCCCTGTCACCTCAAGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /C/TCAACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATTTCCCTGCTTACCCCTATTCAGGCAACTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATCTAATGCGCTAGAT
WI-7870b	85 T C ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTAATTAATCTGTCAGTATTAGAAGGG GTGGGTGGCGGGAATCC/T/CJATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAATTCCTGCAAAATGAATCCAATCAGACTAGAAATTTTAAACATCATTAATGCTGCTAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATGGCTGCAAAAATGAAATCCAATGAGCACTAGATAATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7889c	54 C ---			TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTTAGCTCATGAGTGGAAATCACTACAGGACTGGCCGGGCGCAGGGCCTCT GGCTTCCCTGGCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTTCTCCAGAGCACAAAGAAG
WI-7889b	54 C ---			TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTTAGCTCATGAGTGGAAATCACTACAGGACTGGCCGGGCGCAGGGCCTCT GGCTTCCCTGGCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTTCTCCAGAGCACAAAGAAG
WI-7894c	142 A G ---			AGCCACCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTAATTTATATTGCGTATAC ATTATC[A/G]ATGTAATAATTTGCATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---			AGCCACCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTAATTTATATTGCGTATAC ATTATC[A/G]ATGTAATAATTTGCATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGGCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGGCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGGCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T	---	---	AGACCTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGGGGTGGCTGGGTATTGGGGCAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T	---	---	AGACCTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGGGGTGGCTGGGTATTGGGGCAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T ---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACTAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGCCCTTGGTGGGCTGCTGGGTTATTTGGGCGAGCGCGGTGGTGGT CACTCAGTGGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTCT
WI-7901	271 T G ---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCCT TTTTAAACAACTCCAGGCCCTTGGTGGGCTGCTGGGTTATTTGGGCGAGCGCGGTGGTGGTGCAC TCAGTGGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTCTGTTGT
WI-7926c	150 C A ---	---	CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCAIT TACAAATGCAATACCTA[C/A]ATTTAATACTCTTTGAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T ---	---	CATCCGCATCTGTCAACCCAGGACAGAAATGTCATGGACAAGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTA[C/A]ATTTAATACTCTTTGAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A ---	---	CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCAIT TACAAATGCAATACCTA[C/A]ATTTAATACTCTTTGAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T ---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCAATAGCAGCCAGACCCACAGGCGCGCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]TCTCTCTCTGGAGCAGCAGACTATGGCAGGCCAGTCTGCCACCTG
WI-7947	203 G T ---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCAATAGCAGCCAGACCCACAGGCGCGCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]TCTCTCTCTGGAGCAGCAGACTATGGCAGGCCAGTCTGCCACCTG
WI-7963b	145 T C ---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAATGCC ACAAAATTCATTTCTCTCTTAAGTATTACAATGGAGTTTATCTCTGCTCTAAAAAGTGAAGAAAT TGAGTGAATGA[T/C]AATTTTGTAAATTTAGGATAAGATCCAAAGTTATTTCCCAACTCTTGTTCCTC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAGGCGAGAAGACGGGAAA

[illegible]

WI-8021b	57	CT ---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAC[CT]GATCCC ACGCTTAGAACCTTACACCAAGGAGTTTTCTTGATGATCTCAAAGTCTGGTAGGCATTCGA ACTGGTCTTTCACTTTGAGATCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTGTAGGGGTGATTCGAATCGGTGAATGCCA
WI-8021	57	CT ---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAC[CT]GATCCC ACGCTTAGAACCTTACACCAAGGAGTTTTCTTGATGATCTCAAAGTCTGGTAGGCATTCGA ACTGGTCTTTCACTTTGAGATCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTGTAGGGGTGATTCGAATCGGTGAATGCCA
WI-8024c	206	A G ---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGAGGATCCAGTGGCACTTCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGACCCAGTGTATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG[AG]CTCTAGAACAGCTGGCCCTGGTGTGTCAGTACACAAGGAAGAGC
WI-8024b	206	A G ---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGAGGATCCAGTGGCACTTCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGACCCAGTGTATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG[AG]CTCTAGAACAGCTGGCCCTGGTGTGTCAGTACACAAGGAAGAGC
WI-8077	167	A G ---	GAATGAGCCTTCTAGCGCGAGGGACCTGCTGCTGTTGTCGCTGCAGTGCATTCATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAACTCCTTTCT AAGGAGCTGGGTGTCATGCCCTACAAACC[AG]TAAATTTCTCATCAGATGGATTTTATTTAACGTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAAA
WI-8118f	114	GC ---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGAAACTGGCAATACAGAAATGAGCTTGT[GT]GCTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTGGATGACCACTCCCTTGCTAAGGAAGCTAT TATGTAATTCATGCTGTGAAACTGGCAATACAGAAATGAGCTTGT[GT]GCTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGAAACTGGCAATACAGAAATGAGCTTGT[GT]GCTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA



WI-8118c	44 CT	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGAIC/TCACCTCCCTTGCCTAAGGAAGC TATGTACTTTCATGCTGTGGAACACTGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCCTTCCCT AAAAATCAGACTCAITGTACCAGTAGICTTGAGGACTCAAGCTGAATGA
WI-8118b	88 TC	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACTCCCTTGCCTAAGGAAGCTAT GTACTTCATGCTGTGGAACIT/CGGCCAAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCCTTCCCT AAAAATCAGACTCAITGTACCAGTAGICTTGAGGACTCAAGCTGAATGA
WI-8171d	299 CT	---	---	TTTTCTCTCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8171c	46 AG	---	---	TTTTCTCTCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGJTGCGCAGCGGGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCAATGAAGAGGATGATATAAAACAATCAC
WI-8171a	46 AG	---	---	TTTTCTCTCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGJTGCGCAGCGGGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCAATGAAGAGGATGATATAAAACAATCAC
WI-8171b	298 TC	---	---	TTTTCTCTCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8314b	85 GC	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78 CG	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCCTACTTCTGACCTATTCAATAGGGGTAACCACT

WI-8321	178 GA ---	---	TTTTAAATATGCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTAATTTCAAGAGCTGCTGTTATAGTGAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTCAGAAI[G/A]GTATCTTAGTATCTTCTTA TTTGTATGGTCTAGTTATCAACCTACTTTATAGCTGAACGTGTGGC
WI-8321	178 GA ---	---	TTTTAAATATGCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTAATTTCAAGAGCTGCTGTTATAGTGAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTCAGAAI[G/A]GTATCTTAGTATCTTCTTA TTTGTATGGTCTAGTTATCAACCTACTTTATAGCTGAACGTGTGGC
WI-832b	123 AC ---	---	TATGTACTACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTCTTCCCTCCCTGTGCAGCTTAGA[A/C]ACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCCGAGCAATGCCTACTGGAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGATTAGTGTGATGCACA
WI-8332	114 AC ---	---	TATGTACTACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTCTTCCCTCCCTGTGCAGCTTAGA[A/C]ACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCCGAGCAATGCCTACTGGAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGATTAGTGTGATGCACA
WI-8378b	311 TC ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCAATTAGA AACTGCCCCCATGATCCAATCACCTNTCACAGGCCCCCTCTCCAACACAGTGGGG
WI-8378	308 TC ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCAATTAGA AACTGCCCCCATGATCCAATCACCTNTCACAGGCCCCCTCTCCAACACAGTGGGG
WI-8426	184 TG ---	---	TTTAGCACATATTTAGCATTAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGGNTTCTTTGCTGTGGANGGGGTGGCTTGTGTAACCTCCATTCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61 CA ---	---	TTGAGCCTCCACAATAATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTC[A]CA TCTCTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTTAAAGA AAAAACCTTCCAGTTATTGTGAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTGAT

WI-8450g	55 T C ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450f	108 T A ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450e	125 T C ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450d	125 T C ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450c	108 T A ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450b	61 C A ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450a	55 T C ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8458b	60 A G ---	---	---	CAAGGAAAGCTGTGAGTCTTCATAAACTTTCAAAAGAGTTACAAAAATACGTAATTTTAAAGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCAACCATGTTTATACCTTGTAAGAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGGAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTTATJNNNNNNNNCCCTTGCTTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAAT/jATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTT/jNNNNNNNNCCCTTGCTTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGGTAGTACCTTAATTTTGATAAAAAAAT TAAAAAGCAT/jGJACATGCATATAAAAAATAGATTATGTACAAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATCTCCCTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATCCAGTCTGCAGCTCAGTACCTGT/jTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAT/jTCCAGTCTGCAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAAAACAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT/jCJCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGTNCCCTACTNTATCACTGTGTCTCTGTCTTTTGCTGTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAT/CJCCCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTTGTCCTACTNTATCACTGTGCTCTCTGCTCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATCAAGTATGTTAATGTCACTT GGAATCTACATGGAAAGCCCAACAAAATAACTAAACTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATCAAGTATGTTAATGTCACTT GGAATCTACATGGAAAGCCCAACAAAATAACTAAACTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTCAGAAAGTTGATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTGATTTCCACACATTTGTA/CJAJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAGATTGTGCTAAG/GAJATCATTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTGATTTCCACACATTTGACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACAAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCCCTTNTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAAGAACACTAGAGTCTACACCCAAAGTACAATATGATAAGCAGCCCTCTGCAAGTG GTT/CJGCTGGATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTT
WI-9555	97 G A ---	---	CCAAAGCCAAACCATTCATATGATGGATTTTCATAAACAATTTTATGATCCCTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/GAJCTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTGAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNTCTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGCTACCATATATTGTATCTNCTGCTGGGAAAAACCTTTGGAAAAAACAACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTCTTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTATTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTGGGAAAAACCTTTGGAAAAACACACGCACA TAAGTATCAATACTGAGGGTGTGGACAAGTTACTTCTATGTGTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTAATAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTTCATCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTTGTAACAGTGTATGCTAGACCTAAAAATCCAAGCT TACAACTCTGTGCTTTACCTGATACATTTATCCATTACTTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGCTCTCTTCAGATGTCCTGCTTTTAGTTAATTGTGTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA CTTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA CTTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCCC ATTCACCTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCCC ATTCACCTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCCC ATTCACCTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676a	84	A/C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCCAATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAACTCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCTCGGTGGCTGTGTA[C/A]ATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGGGGGTGTCTTCTACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCCACATGCTGTATTGCTGTCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCTCGGTGGCTGTGTA[C/A]ATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGGGGGTGTCTTCTACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCCACATGCTGTATTGCTGTCC
WI-9756	47 A ---	---	ACTGAAATGTAAATGGCCAAAGGCCACCCAGGACCTTAAAAATCATAAGAAAGTTAATCTGTGGGAAAA GAGTAACATCAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGCCCCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGGTATCCACTCCACAAACACAGAAATATACACTTTTGGGAAG ATTCCACTTAACCACTTGATCTTCACTTTTATGATTTAAACTCTCGGTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTGGCATTGGTTAATGGGCAGACTGGTGCNAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/GTAAATAAATCTCTGGTAGGTTCTATAGCAATGCTAAGTAAGTAACCGCTGGTTCTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCAGGCAGCGGGGAAAATGGATACTTTTCATATGCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTTCAATTTGCCCTTCTCACTCCAAAGTACCAGTATTTACCAATTG[A/CTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCTCCCTTTGCCCTCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTT[C/A]TGGATCCCAAGGAGGA CTCAAAAAAAGTAGGAATGGGAGAGAGGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCCTTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATATATATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAAAGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGGTGTGTTACTTGTATGATGCTGTG
WI-9880c	222 G A ---	---	GAACATAACACCTTTCTTGCATGGAATTTTCTTGATTATGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTATATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG



WI-9880b	157	CA ---	---	GAACAAACACCTTTCTTGCAATGGATTTTCTTGATTAATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTAAGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAATGGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	CT ---	---	GAACAAACACCTTTCTTGCAATGGATTTTCTTGATTAATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTAAGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAATGGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	CT ---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCGAGTTATCACAGTTCTNTTTTGTCTC/CACCC ATTTCCATAACAAAAAGAGCTACACAAAAATNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCAATGAATAATGATTCCAAA
FB25G10b	109	AG ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGTGAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAJN/GJGATTTTAGATCCTCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	AG ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGTGAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAJN/GJGATTTTAGATCCTCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	CA ---	---	ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCAGATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[CA]CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGNCCCTGNNATATTTCTAAACCCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCTATTACCCAGTCTAGGGATTCTG
NIB551	161	CT ---	---	CGTCCCTTTCTTTTGGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGACTTAGGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCT/JTGACCACATACATCGGGCCATTGGTTGATTTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51	GT ---	---	AGCATAGAAAGTGATTTATATTTTAAATGGTTTTCAAGTGAAGTCTCTTTG/JAATTTGTGAGTTC ATTCCTGGAAATCTTTTGGATTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCACAGTGTGTAACCTCTCCCTCTCTGTCATTTGGTTGCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGATTTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATTCCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGAC/TACACCTTTTGTATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCTTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGGTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTTGAACAAGAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGACAGTGAOC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTTCCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCTCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCAGGCCCATNTTCCATGGGACCAGGCTGGCTCAA TGTGGAACTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAACNCTATGTTGTGAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTTGGCTTCTGTCTCCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	---	AGGACACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCATTCCTAACAAACA
ESTC143	29	---	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTTCTTGACATGAGGTCCTTTTAGCAGCATTTCCGG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACAGGTGGCAGCG
ESTC148	42	---	---	---	---	TCITTTGGTTGTCTACACAGACACTTAAAGTACTGTATCGCTGTNATGAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATCTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCTGGCTGCCCTGGGATGGAGCGGGGGCCTCA CCACCAGTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGTACGTTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTGAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGTGATCATCCACCAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGGTGACGTGGGGCCTGAGCTGGGNGCAGTGGCAGTGTCACTGGGCCCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	---	CTCTCGTCGGTTTGAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATATTGGTTTGTACANCGAATACAATCCAATATATAACAATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGTGCCGCGTCTGTTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCCTTTATTCTATTAATAACCTTTTAT TCTCTTTATTCCTCAATAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTTGCTCTGTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGNTTAAATAATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTACAGGGTTATGTCACACCCNTGTCAACCTCAAAACAGATGATCACTCACTTGCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCAGCTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTTCCCTTAACCTTATCAGTCTAGTAAGCNTTCAAAGGAGGAAAATGGGTTAG CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCTCTCCNGCAAAGTCTCCACAAAGACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACCTCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	---	TCTTACTTGGGTAGTTTAGCAACATTTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGAGGGAGGACAGACGNCAGCGCCTGGGTGGCCGCCAGAAAGGCTGGCGTGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	---	TATAGCCCCATCGCTCTCAGTATTAGAATCTGAGAGGGGATAANAGCAATACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	---	CTCCAGAGTCCCTCCTCANACAGGGGAGGAGGTAGGGAAT
ESTC216	49	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTTAAATTAATCACAGGTATTNTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	---	TTTTGTCAAGTAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAAGTTCAT AAACACACCCCA
ESTC219	32	---	---	---	---	GTACACATCCTGGGGTGAGCACACACAGCAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGGAAGC
ESTC22	41	---	---	---	---	TCATTGAAGAAATTTATGGGTTTATTCTTATTCTTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	---	CTTCTGAAGCCCAAGAGAGGGGAGAGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	---	TGCACGTGTTACTCCCGACGACNGAGAGCTTACATACCATATAGAAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	---	TTCTACTTTATTTCATATCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	---	GCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	---	CAAAAGGGTAGTCATATCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCCTCTATTCCTATAAAATAAGGAAGCAGAAATCTG
ESTC3	20	---	---	---	GC CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTATCTTGAGCCGCTTGTCAGGTTTGAT
ESTC31	32	---	---	---	TCGCACACTCC ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAATAAG
ESTC33	25	---	---	---	CAATTTCCCTCAGA AGCACTCCAGCTCCTTGACGTTGNGGAACGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAGAACCATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCCTTCAG
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTTGAACNCTCTCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGGCCAGGGAGCCACTGGTGGGANCCTGGCAGATG
ESTC56	45	---	---	---	TTTACCCTGT GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCA
ESTC57	20	---	---	---	AGT AAGTGGGCCCTCCAGTCCCNCTCTCTGGGCACAGATCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATNGTCCAGACTTCAGGAAAATGATTTCC
ESTC6	27	---	---	---	ACATGGTAAGGCC TCTGCAGCACTTCACTACCAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATG
ESTC61	57	---	---	---	TGGACTGAACCG AGTGATTTTGGCTAGGCGTGGTCTCATCTGTGAATTCACAGCGCAATGACAGCANCTCTCTCCC
ESTC63	20	---	---	---	ACCCACTCAAG ACAGACACAGCATCACACCANAGGGGCCACGGGAGGCTGGGGAGACGACACTTTTCCCTGGGAAA
ESTC69	20	---	---	---	GGCAGCTCTAATC GAGAGGCTAGTCAGGAGGANACCCTCAAGTTTAATCCCCACACTTACTTACTGCTCATCCGT
ESTC7	45	---	---	---	CACITTCGCTAA AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCCTGAGTTGCANGCAGCATGGAGATTGGACACT
					G

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ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGCCTTTGGCGTGACGCTAAAAAGTGTGAAC
ESTC74	49	---	---	---	AACAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTATCATCACNTTGGGTTGAAAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTTCCTGTCCCATCGGAACAGAGTTTCCCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGGGATAAGANCCCCACTCCGCAATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGINTCCTCAGGCTGCATCAGCTGCTTCAGTCTCCAGAACAGAAA
ESTC83	53	---	---	---	GAGCCTGACCCA CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC
ESTC85	28	---	---	---	TTTCACAAACCT TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGTGTTGGGGAGGCTACAGCCTGACCACATTCT
ESTC89	22	---	---	---	TTTGC ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTTCCTTCGCTTGGCATTCTCTCTCCCTCCTCNGCCAGTGTCTCCACCAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTGAGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAAGTTGNAGACGCTCTATTAGTTTGATTCTGTGG
DWU-100	127	CT	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTTCTCCAC/TJGCCAG ATTCTTCAATGATCTTTCACCTAAGAAACACAGCAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAAATCAAAAGAAAGAAAGGCTTAGCTG
DWU-177	77	A	G	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTTCACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC/A/GJGCCCTATTACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213	A	C	---	CAAAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCAATCATGCCAGCTTCTGTCTATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGTAC/TGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC

DWU-252	94 A G ---	---	---	AGTATACAAACATTTAAGCTGGTCAAGGCTACAGATGTGCTACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCCCTCA/GJTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85 C T ---	---	---	GAACATTCCTCTGCAGCACTTCACTACCAAAATGAGCATTAGCTACTTTTCAGAAATGAAGGAGAAAA TGCATTATGTGGACTGA/CJTCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCCCTTTTGCAA CAAGACAAAGCAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAA CTCGATGAATGTGTTGATTTGAGAAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	---	GAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGCCAAGTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAGGTGAATGTTGAGGCCCCCTCACTCCATCACAAGAAAGTGC ATTAGACGGTACCAATTCACTGTCTGTTCCJA/GJGCACTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	---	CTCTTAACITTCAGTTCCTCATCTATAAGAAATAGGGATTGATGTGATCA/CJTATAGCTCAGGTA CAGGACCAAGAAACCCAGGAGCJA/GJTGGAACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCCTGAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	---	CTCTTAACITTCAGTTCCTCATCTATAAGAAATAGGGATTGATGTGATCA/CJTATAGCTCAGGTA ATCCAGGACCAAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCCTGAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTGTCCTCTGTCCTGTTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG/CJGAGA CCCCGAGACCAACTCCTGAGCTTCTGGGCCCTGAGCTGTGCTC
ESTD-ADAA	184 G A ---	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTGTCCTCTGTCCTGTTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTG/CJGAGCACTGAGCTGCAGA CCCCGAGACCAACTCCTGAGCTTCTGGGCCCTGAGCTGTGCTC
ESTD-ANT1	160 T C ---	---	---	TCTCCTGTGCTATTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTCGAAACAAAGAGGCCGAGTGGAGCAGGAGTATTATGCTACGGCGTTACCTT TTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCCTGT
EST10398 2b	188 A G ---	---	---	TGCCTGGGGTGGCAAGGCTGCAACAAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTCACTTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCTTCGGGCCAAGAAAGGTATCTACCA/GJATAGTGCTATTAGGCATTTG



EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGOCACCTCTTATCTACTTGATGATGTTACACATTTGGGGCTTGACTTTCCACACGGGAGAAAG CATTGTTTCTTCTGCTGGGCCAAGAAGGTACTACCAATAGTGTCTATTAGGCATTGG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTCTTTTTCCTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGGGGTGTCCAGGTAGATCCCTTTACQ[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCGCCGACGAGCTGCTGGCACCTGGACGGCGGGCGCAGGCTCACCTCTATAGTGGGTG TATTGCTCCACAA[A/G]TGCACTCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCGCCGACGAGCTGCTGGCACCTGGACGG[G/C]TGGCGCCAGGCTCACTCTATAGTGGG TCGTATTGCTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGGACGAGGTGGGAGGGGGTCTGCTCTCCAGGTCCCACAGACCAGAGAAGGGGCTCAGTG TATCCCCACCCCA[A/G]TGTGGCGCTGGAGATGAAGAGGATTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCCTTAA[A/G]AACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ---			CCAGTGTCTCAATTTTTCAGGTTTAACTC/TGATTACTTTTCTATTCAAACTCTCTGTA AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGCCCAAACCTTGTGGCTGAC TTTATGGCTAAGAGTTTCTACTGGATGCATTAATAACAAAT[A/G]TTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCTA
EST18288 3	121 C T ---			GCTCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/C/TGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGCTC/TTACAGCTGTGTTCTCATGGAGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCAGCACCTTAGGAGGCTGAGGCGGATATCACAGAGGTGAGGATTTGAGACCAAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCTGT AATCCAGGAGGCTGAGGAGGAGAAATGCTTTGAACCTGGAGGCG[A/G]AGGTTGTTGGTGGAGCCGA GATGGCACCATTTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC

EST70523 3	182 G T ---	---	TTCCGGCCAGCCCCCATCTTGGACCCCTGGTCCCTCAGGGGCCACCCGGGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCCGGCGGCTCTTGGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCGGGCTTGGACGGGCCAGCCCTG/TGAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACAGTG
ESTD- APOA2	101 C T ---	---	CCAGGTGTGTGGCACGTGCCTGTATATCCAGCTACTCGGGAGACTAGGCGATGAGATCTTTTGAAC CGGGAGGGCGGAGGTTCAGAGTGAAGTGCATGCTGACATGCTG/GCCACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAGC/TCTAGAAGATACACGAGAC CGAATGTATCAAAATGGACATTGAGAGAACTTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ---	---	AGACATGAAGGAGTTGAAGGCTTACAAATCGGAATCGGAATCGAGGAACAACGTACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCAAGGAGCTGCAGGGCGGCGAGCCCGGCTGGGGCGGACATGGAGGA CGTGGCGGGCGGCTGTGTGAGTACCGCGGAGGTGCAGGCCATGTCTGGCCAGAGCACCGGAGGAGC TGCGGTGGGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	132 C ---	---	CGCTGTGTGAGTACCGGGGAGGTGCAGGCTATCTGGCCAGAGCACCGAGGAGCTGCGGGTGGC CCTCGCTCCACCTGCGCAAGCTGCTGAAGCGGCTCTCCGGATGCCGATGACGTGCAGAGCGCC TGCGAGTGTACAGGCGGGGCGCGGAGGGCGCGAGCGCGGCTCAGCGCATCCGGAGCGGCTG GGCGCTGTGTGAACAGGGCGCGCTGCGGGCGCGCCTGTTGGGCTC
ESTD- ARSB	126 A ---	---	GGAGAAATGGAGCTGTGGGAGGAGCGCTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAGGGGTGAAGAACCGGGAGCTCATCCACATCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACCAATGGCACAAAGCTCTGGATGGCTTGACGTGTGGAAACCATCAGTGAA GGAAGCCATCCCGCAGAAATGAGCTGCTGCATATATTGACCCAAAC
EST36770 4	144 C ---	---	TGTAGCCAAAGTCACTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGGCTGGGCTGACCAAAATATACTGGTTTCCCTTCTCTTCTGATCAT TCTTACAAGTTATCTCTTATTGGAAGGCCCTAAGAAGGCTTATG
EST26021 1	137 A ---	---	TAATGTAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAAAATGA GCATTAGCTACTTTTCAAGATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29 A/G ---	---	GGGCAACATAGTGAACCCCATCTCTACATG/AAATACAAAATAGCCAGGTGTGGTAGCAAG TGCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCTGGGAGGTGGAGGCTG CAGTGACCAAGATGGTCCACTGCA

ESTD-BCI2	116 A G ---			AGTGGATTATAACTCTCTTTCTCTGGGGCCGCTGGGTGGGACGTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAA/C/A/GGGTAGACAACCGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGGCTACGAGTGGGATCGGGGAGATGT GGCGCGCGCCCCCGGGGGCGCCCCCGCAOCCGGCATCTTCTCTCCCA
ESTD-BCR	69 C T ---			CAGTGGCTGAGTGGACGATGACATTGAAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GA/C/TJCAAAGAGGTCACTTCTGTGTCCCGGAAAGGGAGGCAGGTGACAAGCTAATCTCGCTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCTGGCACA
ESTD-BRCA1aa	119 C T ---			AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAAATAATGCTGAAGACCCCAAAAGATCTCATGTTAA GTGGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGATAGCAGTATTTCAT/C/TJGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTTGAAGTTAGCACTCTAGGGAAGGCAAAAAACA GAACCAATAAAT
ESTD-BRCA1bb	139 A G ---			ACTAAATGTAGAAAAATCTGTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTAGAGCAACAATTAGCCGTAATAAGATTAGAGAAAAATGTT TTTAAAG/A/GJAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD-BRCA1cc	126 A G ---			ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAGAA/A/GJAGGA GAGCTTAGCAGGAGTCTAGCCCTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCTCAGAAAGAGAACTTATCTAGTGGGATGAAGAGCTTCCC
EST512120	122 A C ---			ATCTGAGCTGCCAATAAGCTTCTTGTTCTACTTCTCTCTCCACAAGCCCCCAATTTCACTTTCTCA GAGGAAATCCCAAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACA/A/CJAAGGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGCTGGGATCCTCTCCCTTNGJATTTGCTCGGGAAGCACATTCAAT CAA
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGCTGGGATCCTCTCCCTTNGJATTTGCTCGGGAAGCACATTCAAT CAA
ESTD-C6	31 A C ---			CCCAGTCAGTTGGGGACAGCCATGCACTG/A/CJGCCCTCTGGTAGCCTTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST201182	119 C ---			GTTCCGAATCCTCTCTGAAAGTGGCCGGTTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTAGGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCACTCTAAGCTCT GAGAGCAAAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST530186	67 A G ---			ACAATCCAGGTACACATTCAGAAAGAGGGGGTGGTCACTGAGCCTGGGTAGGTCCAGTAATCCA /A/GJGGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGAGTGCCAAACCCATAGGGCTGGATACAAAAG ACAGGCAAGGAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCAATTACCTTCCCTTCCAGAGGACCTGAAACGCTGTTCCCAACCCGA GGTGGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAA
ESTD- CB24	145 A ---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCAATTACCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCCAACCCAGGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCCGACACGCTGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACACCCGACGCCCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	GTTTCTTTCAGACTGGCTTACCTCCGGTAAGTACTCTCTCTTCTCTCTCTCTCTCTCTCTCTCT TCTGCTCTCGAACCCAGGGCATGGAGATCCACGGACACAGGGGGTGAGGAGGCCAGAGCCACCTG TGCACAGGTGAGCTACATGCTCTGTTCTGTCACAGAGCTTACCAGCAAGGGGCTCTCTCTCTG ACCATCTCTATGAGATCTTCTAGGGAAGGCCACCTTGTATGCGGTG
ESTD- CB27	125 C T ---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACCTGACCTCTCT TGATTTAGGGAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTCTGTTCACTCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTACCTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATATGTA TTTTCTTAAACAATAAACTTGAAAGTCCAAAATTAAGTCTTGATCCATGGAGTGCAGAAATAAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATCTTGACATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTCATGCACTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGCGTGGTGGAGGTGTCACCATCCCGGCAGAGAACAGGTGACCCACTATGCA/GICA GGTTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTGGCTGAGCAGGGCGGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	AAAAAACAATTTAACACCTTTTCAATCATATACACCAATA/CJATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAAGTCAATCTAAATGTCAATACTGATTAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATACATATCTGGATTAAATATGCCCCA TATCTGCACTG
ESTD- D17S33b	169 C T ---	---	CATCCCCAAGCCCATCCTTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTGTGTAGTGTGGGGCTTTGGTTTCAGTTGCACTATTGCGTT ATTGAGATTGCTTGTCTTCCACCTGAGCGAGCTC

ESTD- D17S33a	75 CT ---	---	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTGGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGTCACACATCCAGGGGCGCCCTACCCCTTGATGTCATGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTCTTGTTAGACGGGGCTTGGTTTCAGTTGCACTATTGGCTT ATTGAGATTGCTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCATGCTATGTAATCCAGCTACATCGGAGGCTGAGGAGGAGAAATTGCTTGAACCC[A /G]GGAGGCAGAGCTTGCAGTGAGCCAAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATAATTTATCTGAAAAAGTCGAGTTATTGGTCATCACATTGG AATTTTGCATGATTAATAAATCCAAATAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTATCACATTAATTTATTGGTAAGCCATACTAAATCTAAAGCATGTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGGTGATGTTTCC[A/G]GGAGCCTTGATGTCATTCTGTATCTCCT CAGGTATCCACCTTGAGAGCTACTTTTCAAAAACCTCTACAGCCGTTGTTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 CT ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTCATAGTGTCTGTTTCGGTCTTACGATGG CAGGTATGAAATATAATACTGTCTCTTTATTGGAAAGGATGCCTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTCATAGTGTCTGTTTCGGTCTTACGATGG CAGGTATGAAATATAATACTGTCTCTTTATTGGAAAGGATGCCTGGTATGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACC[A/G]GTCTCTCTACATCCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGCAAGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATT[A/G]TCTGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGAGCAGAGCGGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGCAAGTGTGGCTCAAGCAGCTGCTGGGCTCCAC[A/G] GJTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGAGA CAGATGCTGATTATCTGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAAGA CCTCCTGATTGAGGAAGGGAGCAGAGCGGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---			TCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCCACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGIC/TTTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCTTTGGTCAGAGGCTGCCGGGAGCCAGGAGCTGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCAGCCACACAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCGACAGCCGCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTTCAGGTGGC/TTACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---			TCTTTAGGATCCGCATCTGGCGCTGGTTGGGCATCGCTCCGCTAGGTGTACGGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGTC/TTGGGGGCGGTGCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTTCTGCAGCAGTCTCCGCATCGTGACT
ESTD- ETS2	43 A G ---			ACTCACAGTCTTTAAGTGAAATGGTGCAGAAAGAGGCACC/AG/GGAAGCCGCTCCTGGCGCCTG GCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACAGGAAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAATTAGTTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTT/AG/GTCAAACCTTCATTTTTTTTTTC ATAGGTATGTCCAATTTATCCAGCAATTTGTTAAACAACAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAG GAAGCTTGCAAGCTCATGACAAATTTGAAGCTGACAATACACAAGGAAGAAATAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGTCACTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G ---			CGCAGACCGGTGAGTGGGGTCCGGAGTGTGGAGGGAAGGAGGGAAGTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTCTTGACAGAGAAAGGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGGAACCTCTGGTCCGACCGGTGTTCTGCTGCCCTGTTTCACTGTCTGTCTGCGCGAGT/CT G/GACTCTGTCCCGGAATTCGAGAGCT
ESTD-GCK	88 A G ---			GTTTATGTCATGGCAGCTCTAATGACAGGATGTCAGCCCTGCTGAGGCCACTCCTGTGCACCATGAC AACCACAGGCCCTCTCAGGA/AG/CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGCGCGCTGAGCCCCAGGGAAGCAGGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAAAGAGACCGGCTC/AT/
ESTD- GNAT2	56 A G ---	---	AGGATCCCAAGGCCCAACTCCCGAACCACCTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCT ACAGGTAAG
ESTD-HT2	154 G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCAAC/AG/GGGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTTACAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT5	149 C ---	---	GGGCTAAATTTCCGAGCAACTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGCAGAGAGATAAAAGGATAACCTGGGTTTTCTGTGC TTTGCTTCTTACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACACAAGCCCCAGCGAGAAATTGAACCTCGCGACCCCTGGTTTACAGACCAAGTCTAAACCCCT GAGCTATGGAGCCCTCGTCTGTGTGGTTTTCTTCTTTCATCTTATAGATTGATGTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTAGCTTGAGTAAATCCAGGATATTCTCTACAAAATGAAA ACATTTCTGCTCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCGCTTGGGA CTTTGAGTCAAAATTTGGCTGGACTTGAGTCCCTGACCAGCAAGAGAAAGAG/AG/CCCCAGA AATCAGGTGGGACGTCGGCTACCGCCATCTCCCTTCTCAGGGAAATTTTACAGGTAACCT
ESTD- IGFBP1	43 C T ---	---	ACCAGTGGAGCCCGCTCAITGCACGGTCTTGGCAGGAGTG/C/TTCTGGGAGAGAAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTTGGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATTTGCCCTACATTGTGTGAGTGACGGGCGAGTGGTGAATCCGAGAGTGTGGGG TGCACGGACATAATGATTTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTAATTATTTATTTATTTTATTTTGG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCGAGTGGA/AG/CAATCTCGGCTCACTGCAAGCT CTGCCCTCTGGGTTTCATGCCATTCTCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAAATTTTGTATTTTGTAGTAGAGACGGAGTTACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGTGTCTCTGCCCTC/AG/GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGACCCAGGCCACCTCTGCAGCAGGGAGGAGTGGCTGGGCTGTGAAGCATG TGGGGTGAAGCCAGGGGCCCCAAGGAGGGCACTGGCTTACGCTGCTCAGCCCTGCTGTCTG/AT/
			TGCCAGATCACTGTCTCTGCGCATGGCCCTGTGGAATGCGCTCTCTGCGGCTGTGGCGCTGTGGCC CTCTGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGC



EST45311 0	151 C T ---			GGCCTCCTCTCCAAATTCTGTCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TJACCTCTTTCAITTAACAGCCCTATTCAATGGCCTTTTCTCTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---			TGCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCAACAAATTAACAGAAAT CCAGTTATTTTC/JGJCCCTCAAAATGACAGCCATGGCGGCGGGTCTCTGGGGCTCGTGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---			ATGCAGGATGAAGGTGGACAGGGAGG/JTGAGGGCCAACTGTCTCCAGGGCCTGCAGATGTGCG CTGGACTATGGGTTGTGACCCCACTGACCTCATGAGCATCAGGG
EST62782	149 G T ---			ATACTAGTACAAGTGGTAATTTTGACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTAAATGACAGTGGAAG TTTTTTTTCTCTG/JJAGGTGCCAGTATCCAGAGTTTTGGTTTTTGAACCTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGCTTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT10a	133 A G ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTA/J GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8b	231 C T ---			ACCTCAGCCCTCCCTTAGCCGCTGAGGAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCA/C/JJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---			ACCCTACCCCTCCCTTAGCC/C/JJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGAATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---			CACTTGTGTGTCTAGATCTCTCAGTGGCGCCCTCTACTGGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/JJGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGGCCACC CCTTCTCTGGCCGCTCTTGAGGTGTGG



ESTD- LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGTAACCGTAGCAAAACTGCATTGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCA/GJGGAGGGCTTCCCTTACCACCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGCGCAAATCTGACACGTGTGCACCCAGGTGTACCAATTAGGTGAACATGGCTTCGAG AGAGTTGACJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGGCGAGGAGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G ---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTC/GJSCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTTGGCCTGTCTGCTGCTGCCTGCA AGGGTTTGTCTAATCTCAATTCATGTCTCTTCATCTTTTAGTC/TJAGCTGTGGGTTTGTGTTG TTCTCTGTTTGTCTAGTCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCACAACATTTATAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCAAGCTGTCTGCTAGCTC/TGAACCTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTTGGTGAAGTTGCTGATTACC/C/TJGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCTAGTACCAGATCCCACAGACTGATATGGCTGGT
ESTD- NFKB1	107 A G ---	---	AACATGGACTGTATATTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTT/GJGCCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGGTTTTGGAGAGGTTATCA
ESTD- NPPA	45 A G ---	---	TGTCCTTAGGCCACGCCCTGCTTGTCTCCCTGGCTGTTATCTTC/TAG/GTACTGCAAGAGAACACA GACAT
ESTD- NPAS	202 C T ---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACCAGATAGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG/ C/TATCCCTGTGTTTTTAATAAAAT
ESTD-PAI1	100 A G ---	---	GCCACCACACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/GJGTCAGCCCGTGTATCATCGGAGCGGCCGGG CACATGGCAGGGATGAGGGAAAGACCAAGAGTCTCTGTGTTGGGCCCCAAGTCTCTAGACAGACAAAAAC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCAACGAGTCTCTTACCAAAACACGACTTATTGCTGTCGAGAGGTACAACCCGCTAGA ACTTCTCCTAACTGTAATTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACCTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACCTTCTGTGTTCTAGAACGTTTTTCTAG GACTGGCAGTTTAAAGCTTTCACCTAGGCTTCTGTATACCATGCC
ESTD- Per/RDS	74 A G	---	---	ACCTACAGACGTCGCTGGATGGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGA/GGAGCGTGCCGGAGACCTGGAGGCT
EST68308 5	29 C T	---	---	GGAAAGAGATTTAAGAAGCTTGAATTGGAGCTAAATCTCTGTTCTTGGTGGGAGAGTTTCATGTC TCTGCCTGAGTTACAACAGAACTCTTGTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045 6	39 A G	---	---	GGAAATTTAAAATATTTAAAATACCTCCATTTGCTTGA/GTCTTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGACCTTATCAT
ESTD- PXMP1	88 A G	---	---	ATGAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAAGGCTTCTTTTTTTTA ATGAGAAAAGAGGGGAAAAA/GGAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC AGATTTTGAAATCATGTGCTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTAATCTT CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGGGAGAAGAGCGTCCGGAGACCTTGAAGG CCTTCTGGAGAGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCGGAGGCGCAGACGCGAGG CCAGGCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAAGACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-RDS	127 A	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCTG/CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
ESTD- s14544	94 G T	---	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/AC/TTGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST52908 0	45 A C	---	---	AGGAGAAGCTGAGGAGGGGAAGAGACAAAGAAATGACATTTGATGAGTGAAGATGTC/TTGGCTCAG GATGCCGGAAATGAC
EST19590	55 C T	---	---	TGAAGCTTCTGCCAGCTTGCAATTGTTTCTAGGAGAACCT/CTGGCTCATACCTTTATCTATAGCCTT CCCCTAGGCTT
EST76136	39 C T	---	---	TGAACACCTGTGGTCCGAGCAGGTGTGTTTCTCTGGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCTGGCCTGTTGTGCACAC/CTCCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCAAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SPTB	176 C T	---	---	

ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTCTCTCACCCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THFB	125 A C ---	---	---	TGCGGCCTTTCTCCGGCAGGGTAGACTTCTTACTGGCTGTTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACAGAGATC/A/C/TTCAT CCACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGAATTTCTGCCACCCGCAACAAGAAGTCTATGC CAAGGCAGAAAAGCTGGTCTCATGGGCAAAATCAATGTCCTCCAGATTTCA/G/TATCCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCAATAATTGATGTCGTAA CATGGGTGTGATCCATTTTCAITTTGGCCATAGTCCCTATGGGGATGACA
ESTD-TYR	122 G T ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATGATTTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATGATTTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC/A/G/TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCACCGTTATATGTTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607	0	105 A G ---			CTCTGGATGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCTACTGGAGAACAAAGGACAGCCAC/A/GTGGCGGGGATGGCCGGGGAGTTTC TGTTGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGGGTGCCATGCTGAGATGTAGATGGGOC
ESTD-VWF	36	G ---			AGGTAGGAAAGCAAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
EST71770	6	189 C G ---			AGCACACCTCTCAGTCAAGCCTCAGCACCATGCTGTCTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGACACAGAGATTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGACTGTGATTGTGAACAACAAGAGAAACCACTGCAGATCCAGC/GTGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD-TNFab	152	A G ---			TTCTGCATCCTGTCTGGAAGTTAGAAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTC/A/GJAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGTCCTCCAACTTTCCAAATCCCGCCCCCGGATGG
ESTD-TNFa	88	A ---			TTCTGCATCCTGTCTGGAAGTTAGAAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCTCCAACTTTCCAAATCCCGCCCCCGGATGG
EST52418	6	113 A G ---			CAAAATACAGGGTCAACTGCTATGATGTGTTTGGAGCCAGTCACCTTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTCAGGCATACACT/A/GAAGTGAAAACTGTGAGTG TGG
EST13586	3	89 A G ---			CCCACTCTATTTGCCAGCCCCAGGACAGAGCTGATCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/A/GJGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTCTTAGAGACTGCGAGAAGGAGTGGCTCCTGCTGCTGCC CCGGTCACTC
EST51976	7	123 A T ---			AGGCAGAACTGGGCCCCCATGCGGGGACGTGGAAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG/A/TJCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGAGGAGGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGG
EST11458	6	140 A G ---			CCACTTTGGTAGTGCAGGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCC/A/GJTAAACAATTCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGOC

ESTD- AT3aa	60	CT	---	AGACCTCAGTTTCTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC[CT]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106	CG	---	CGGTCTTCCTCCAGGTAATTGTCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATTAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTA[CTG]GTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	AG	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGCAATTGCCGGCCCTCTCGGGGCCCTGG TCTCTCTGGTGTGGTAGTCTGGAGTCAACGGTCTCT[CTG]GTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGGTCCCTCCAGTCCGATGGTCAACCCGGACACAAGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120	AC	---	AGTGACTTCCAGGAATGGCTACCAACTTGCCTTCATGGCCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGG[CT]AACCTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATAGTGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112	AG	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTGTCACCTT[CTG]GGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGTAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	CT	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA[CT]TGGACTCTTCTACTGCGAGGACAGAACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150	AG	---	GCCGAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGTACCATCACCTTCTCTCATGAAAAAC TGGGAGCGCGGCAT[CTG]GTGCTCATGCTGTAATCCAGCATTTTGAAGGCTGAGGCGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACT
EST12274 0	135	AG	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTGCTTCCAATAGAGCCCTTACCAAGTGTAT TACATAAAGAAAGTCAAGTGTTTACTCCTCATGACCAATACTTCTCCCTCTTAGGATGAGGTG[ A/G]TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91	G	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGGGGCCCTGTCTATC CAGCTCACTCATCAATGGGCGCAGTCAAGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTACATTTGTGGATTGTTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGCTTTGGCTGCTGTGCTGTGGGATAATTTGAAAGAGATCTTTTGCCAGTCCAATGTCTCTAGAGATTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATTTGATTTGATTCTGTA
ESTD-RVRI	109 A G ---	---	CTTGTGACGGGAGGTACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCCCTGTGTACAGTATGACACGCGAGACTTGTCTACTATAGAGAGGGGAGCTGTGTGCACTCATGCCCGCTCCCTGTGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACTGTGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCTCCCTTCTCTTACTCTCTGCTGCGAGGATGTGCGAGCGTGTGCTGGAGTAGOCCCGACTCTTTGACGGTGGCATCTGAGACAGTGAAGAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C --- 62 C T ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCCAAGTGTGCATGCACGCTTAACCTCTGCACCAATGGCTTCCAAGGCCGTAGGGGAAGTGGGGATCTAGGGGATGGTGAGGAATGGGCCAGCCAGTCCCGCGGCTGGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGGAGATGGGCTGGATGAG
ESTD-PBDA	103 A G ---	---	GGAGCCAGGAGCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGAATCTGTCTGTCTCCGACCTAAGCGGAGAGCCTCAAGAGCCGAGCGAGTGGG
EST12839 3	122 A G ---	---	CCCTTCATGCCAGATGGAAATTCAGATCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGAGGGGAGGACTAATCCAAAGTCTCTACCCGAGCTTGTCTGCGCATACAGCGGACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGAGTCAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAAGGAACTTGAATGTTATTCAACTGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCCTTGGATTTCAGCGGCACAAAGGCTCAGCTGAACCTGGCTTGAJGJCCAGGACCTGGCCCTGCACTCTCTCTGTTTCTCTCTCTCATCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCACTCTCCAGGCAAGGCCACGATCAAGCAGTGCACACGGGTCAAGTGGACCAAGTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCGCTGTCTCTCCCTGCTGCGGGGGCCAAACCCGGCTTCCA
EST54419 8	88 A G ---	---	TGAGGCCATTGGGACAGTGTGGCGCTCTCGGTCTCCACTCCCTGAACATCTGCACAAAATCGGCTGCTCTCTGCCTAATTGAATGATATTGTGTGCTGTGGGACCTGAGCACTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTACAGATCTGCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTGTCTACTAGTCCCAAGTGAA

ESTD-PS-1	99 A G ---			GGGAGTAAACTGGATTGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACACCATAGCCTTGGTTCTGAGCCATATTAATTGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---			GGCTGCCAGGGTTCCGTGGAGGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGGTCACTCGTGGCCATGCGCTGGAGACTCCAGACCATGACCAA CGTGTCTGTAAGTCTGCTGGCCGACGCCGACCTGGTGATGGACTCTGCTGGTGGCGCGGGGCCA CCTTGGGCGC
WI-567b	48 A G ---			TCTCAGACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTCTGAGCCCTCATCTCTTTA CAGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTCTTCTCCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTCCCAAGGTGATCTGATGCTACCATCTTGTCTTCAAGCC
WI-801c	58 G T ---			ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTCTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---			ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTCTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---			GAAATTCACCTATACAAGAACTATTTCTCTAAATTTACATTAGTCTCATTATCTGAAATATTAT TTTTACA/JGTACCCCTTGTATTTTGTATTTGATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAAATGTCTAAATACTTTTGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71 C T ---			AGGAAATGGCTGATACCTCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/JTCTTAACTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---			TAAGGGCTGTCTTCCCCAGAGGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCTATGAGGTAACTTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAGAGCAGCAAGGAGAGAAAGGAAGT

WI-2625	98 GA ---			---	GGGAGTCCTGGCTGTAGTGGTAGACAGCAGCTGAAGGATGGAGGAGAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAGGCTTATTTAGGA/GA/JCAAAATTGATGATCTCCTGAGGACTCGCAG AAATTACAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 GA TAGG	TGACCTTCTTA GTCTTCTCTTA		GCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCTAGTCTTCTTATAGG/GA/JACCCTGTGATT ACACTTAGGGCTACCTGGATTATTTAGAACAATC
WI-2939	72 GT GTGCCITT	GGCTTGCTCA		CTTGTTGAGGG AAGGCTTG	CCATTGTTAGGTTGGTGGGTCACCTTGTCATTCCTCGCAGCTCAACAAAGTGGCTGTCTCAGTGC CTTTG/JCAAGACCTTCCCTCAACAAGATGTCTTCCATGCTCCGTTCTTTTGAAAAATTCGACT TTATCCTGAAAAACTCAGCTGAGTGTATCTCCGGTATAAGCCACTCCTG
WI-3203	99 GA AGACGAG	GGTATGCCGC		TCAAGTATTGC CTTGTTGG	CTTGCTACCATGCAATTCACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGAG/GA/JCCACACAAGGCAATACTTGAAGTGAATGGGA GAATAAGATTGTTGGATGGATGAAAGCAGAGAGGAGATGCTAAAGTGA
WI-3473	101 AG GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA		CCTGATGTCAC CAACATTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAAAGGACATTTAGCCCTAGGGA/GA/JTAGAAAAATGTTGGTACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA/GA/JGCGAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCGC
WI-1796b	29 AG ---			---	ACACACTTTTCTGTATGCTCTTCATCAAA/GA/JGCGAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCGC
WI-1796	29 AG ---			---	AGTGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAGATGGGGTGAAT AGTCACATTAGGTATTTCCAAATAA/GA/JAAAAATGCCCTCTGAAAAATATCTCTCCCATGTCCTGTC TAAATATAACATTTTCCC
WI-4360	93 CT AAATAA	GATGTCACATT AGGTATTTCC		GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGGAATTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTCT/JGGGTAAGTGAAGTGGTTTTCACACCCAAA
WI-1959b	87 CT ---			---	GTTGTCCCTGTAGCAGACAGAGAGGCA/GA/JAGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 AG ---			---	CTTGAGTATCGTGGATTGTTGTATACACAGAAATGGGAGAGCTGGAACTAATCCCCCATATACCA AGGGACAAATTGTATCTGTTTCTACAATTATACAGTAGGAGACATTTATGTTCCATGACAATGGTAAT TTTTAA/GA/JGACAGTTTTTAATTGAGTGAATTACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC
WI-1980b	140 CT ---			---	



WI-2015b	190 A G ---			TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTTGCAGATAGCATGACCATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTGCTATAAACTCTACATGGTGTCTTTCCAACTTAA/GJCATATACTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGAGAGAGATGGCTGTCACTCTACCAGCCAGGAGAGAGC/TJACATTTATTGGTAA TCCTATAAAGTGCATTCTTTAAAATTTGATTTACTTTAGA
WI-754	22 T C ---			GAAGGCACAGGAGAGAGATGGCTGTCACTCTACCAGCCAGGAGAGAGC/TJACATTTATTGGTAA TCCTATAAAGTGCATTCTTTAAAATTTGATTTACTTTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---			TAAATTTAAAATGGGGCCAAATACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/A/GJCTAAAGTTATTAGTCTCAGAGCCTCACACATTTCTCAGTACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---			TAAATTTAAAATGGGGCCAAATACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/TJGTATCTAAAGTTATTAGTCTCAGAGCCTCACACATTTCTCAGTACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---			GAGCCTTTCTAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGTCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C ---			CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCAGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---			CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCAGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---			CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCAGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A ---			CGGGACAGAGACAGAGAGAGATTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5c	177 C ---			CGGGACAGAGACAGAGAGAGATTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5b	159 A ---			CGGGACAGAGACAGAGAGAGATTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCACTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACAC AGTTTTACGTCCAG
WIR-5a	37 A G ---			TAACCTGAAACTTTGTCTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AC]
WIR-6	63 A C ---			CGCAGTCTGGGGTGGGCGAG
WIR-7	12 C T ---			TTGGTGACTATTCTJAAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46 C T ---			GGCGTCTATGACTATCCTGGTCACTGATTGACTAATGCTGCTGCTGGCCCTTG
WIR-2	56 C G ---			AAACAGAAAAATAGAGGTTATAAGGATGGAACCTAAAAGTTGTGAGAAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATAACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G A ---			TGTCTTGCTTATGCCTGCCTCTTTCGCTTGGCAGGATGATGCTGTCATTAGTATTCACAAGAAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCATTCCTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACTGTTCTCAGTC
WI-18694	41 A T ---			GGTCATTTCCTTTTATCTGTCAGGAGCCAGCTGACTTJA/TCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A G TGC	CCTATATTCA AGTTGGAAA	TTGTATTGCTG CTTGCAAT	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTTATGAAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]GTGTGCACTGTCCAAACACAACCTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCCAAAAA	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGATATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGTTCCTCCGA GGGTAC	TGAAGGCOCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACCAACACCAAGGGCAGTTGGGCTTGAAGGAGCC CTTGAGGAAACACCGGTTCTCCGAGGGGTAC[C/G]CCAGCAGGGCCTTCAAGCTTAAAGTCG
WI-18673	29	A G ---		---	TGTGGGCAAACTTGTTTTAAATTGCAAAAC[C/G]ACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGATTGCTGACTTTGTAAACATATGAATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121	T C	GTGTTGGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTTATTTGGAGGTTAATCTCTATAGGATATGAAAGGATTGAGCAACGATTGAGATT GTGTTCTCAGGAGGGCTCGGGCCAAAGTGTGGGGTGGGGGTGCAGAG[C/G]GTGCTCTCTTC
WI-18538b	91	T C ---		---	AGTGGATTTCGGGAOC
WI-18538a	59	T G ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAA[C/T]TACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C T T C	TCATCTGATAC CTTGTTGAGAT	AACCAGGATA AGGCTACAACT ATTT	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAACTCCCGAGATTTCTCTTTATTT TTTTATATTTTCATTTTTCATCCTAAATTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
D49493	159	A T T C T G G G A A T T			GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTGAGATTT[C/C]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACCTTT
EST10030	7				CAGGACTTGTGTGCTGAGCTGCAGACACAGACAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATAGGGGGTCTTTCAATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTTA/TGGCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10052	2				TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT[C/T]CATCCATACCACCCTGCTGATTTG
					TATTTGGCTCACTTCTGGAGGCTG[A/G]AAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCATAACCTGGTGGAGTGCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A
	24	G A	GAGGCTG	TC	

EST10605 2	118 C G ---			CTTCGTAATCACAGTTCTGTATTCTATACAAAAAAGCTTTGTTTTCTCTGACAAAAGTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGTG/GJTTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGAAAT TTGTTT	CATGTGTCAATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATATATCTT/GJAA ACAAAATCTTTCTGAAAAATTTAGCTTATGAACCTATTACACTGCAACCCAGAGAAGGAGCAC
EST11260 8	101 G T ---		---	TATGGAGGCCAGAGAGAGTGACACTATATGTGGAAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATATCAATTAAGAATGAAG/GJGGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---		---	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGGAATTCAGCTTTACCGCTTTCTCTCATCTGCTGGTG/GJTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	CCAACTACTT TGGAGCCT	TCCAGCTTTCT CTAAAACTCC T	GAATCTGGGTATTAATAGCGGTGCCACAGGACACATAGGAAGAGCATCCAACCTACTTTGGAG CCCTA/GJAGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGTAGCCAGACCAA AAGGAGGAAGAGTGGAA
EST11772 6	74 A G ---		---	CCAGGAATAAAAAGAAAGAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA/GJGACTATTTCTGACTATAAGTGAATAAATACATTTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---		---	CTTGTCATTTATTTTGTCATGTTGTTCTTAAAGGCTTGTAAGGATAACTTGGAAATGTGGGAAAC ACATAGATCCAGAG/GJATTAAAGGGCTGGAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGATCTCAATAAGCAGCTCATTTTGATTAC/GJAGGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAGCCTCCACAGAACTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCTGGAT	GCCTAGTAATTTCCAAAGGAACATGTTTGTATATAACACTCAGTACAAAGTCTGT/GJATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ---		---	GTGGAAAAATTTTATCTGTTACGCTTTTCC/GJATTATATTATCTTGTCCTTGATTTCAGCACCC CACCCGATTTCAGGCAGTCTTTCTAAAGTGTGCCCTGTGAGCTGTTAAAAAGTCTCT
EST12492 1b	95 A G ---		---	CCCTAGCAATGACTTGGAGTTGTGCCAATTACCAAGTTACATACTGTTGCCAAAATTAAGCTCTC TCCCCAGAGGCATTAACTGAGATTAT/GJGGAAACGCACAGCAAAAATTGACGATGCAGCTTTTA CCTTTTA
EST12492 4	25 A G ---		---	ATCTTGAGGTTCTGGCCTGTCAG/GJAAAGTGACATCTTTTACTTACCACAGGTCAGGAACCTTAT AAAGAAAGTGTGTAGAAAAGATATCAGGTACAGACTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCAICIGCAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAGAAATGCTCACGGGGAAATGACCAATTTTAAAGGGCCATGTG GTCGTGAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAATAGAAATGATCGGTAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATATATCCCAATGACAGTGTGCTGAGATTCGATGATGTCGAGACGAG
EST12620 0	67 A G ---			TTTCTCTCTCTCATTTTATTTGTTCAAACACTGTCTAGTACCAACATTGTCCACCGGCJA /GJTTGAGAAATACAATATTGAAGAAGAGTCACTGCCTGCCCTGGAATAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTTCCTCAGGATTCAGICAJCTGTAGCTGTGTCATGAGTTCTCATCCATGCTCCACGG GTTCTGGGAGTACCGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCATTGGC
EST12941 8	23 T A ---			TCTCAGCTCCACCTGACCTGCAIT/AJCAACAGCCCAAGTTATTTCCACAGAAATTTGTTGCGTTTCA ATGTAGTGTTAGCTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G A T A C T G T T	GGCTTTAATCA TAACCTAATA	TGTTGCTCTGT GGTCTC	AGGATTCATGAGGCTTTAATCATAACCTAATAACTGTTAAACAAACACAJ/GJCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTCTCTCCTCCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTAAATGAAGCATAATAAACAGTTAAATCTGTTAAACAAACACAJ/GJCTGTCACTTG GTGTAACCTCCCTAAATCAGTCTTCTAGGGCCACAJCTGGAGCAGAAGCAGCTTCCCACCCAAAG CACCTCTGAAC
EST13117 8	66 A G ---			TGCTGTCTGTCATCAGTCTTTTAAATAATTAATGCTTTATACAAATTGACACCAATAAAATGACAJA /GJATTAAAGTTTACAATTTGAGAAGCTGACACGTTGCTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 8	44 C T ---			TCTGCTTTAAAGATTCTCATAGCTGCTTGGTTTGTCTTCCJC/TJAGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCGAGGCCAGTCTCCTCAGTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAATAGTCT GGCCATTI/GJGACTAACCAAGTCTACAAATTTACATATCCGTCACATGAGCATATACCAAG TCAGAGGAAACAAACATG
EST13230 6	72 G A A G A C G C	GCTCAGATGTG ACAGAGA	CCGGCTCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/GJA/TCTCTGTACAGAGCCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C A G G C C T	AACAGAGGGTT TGACAAAAGA	G	AAAGATATAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACAGATTTTCTCAGG CCTT/CJTTTTGGATACCCTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGTATATAACCA

EST13278 2a	51 A G G	CATTACCGAA CAATATTTTAG	CATATTTCTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAAGCTCCAAACCTTTTACCAGAACAAATATTTTAGGAGAGATTTGAAATATAT TTCTGTAGTTCTACCAACCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGT	GCTCACTAGATGAGCATGACCAAAATATTTAGATAATACCTGTTGGGAAAGTGCTGAAATTAAGCC TGCCTGAGAAATCCACACACATTTACGTCCAAGAAATTAACCTTCTCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39 A G CTT	CAATTTTGTAGA AGTTGGGTTT	AAATCATTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTGTAGAAGTTTGGGTTTCTTJAGJCTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTCACTTAAAGACCTAAAGACAAAGTGGTATCACATACATATTTTGT ATGTGGGGCTTTTGTG
EST13518 2	45 C G ---		---	GAAACATCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTA/C/GJACTTTTAAAAAATTACCTCA ATGTTCTCGGAGTCGTCCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	66 A G ---		---	CAGGTTGGTGATTTCTCACTAGGAGCTATTTTGCCTCCATCCCAACCGGAGTGCTGGAGACJ/ GJGTTTGTATTGTCAAACTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C ---		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAJ/CJGCACACAAAGGAATAAGGGAGAGGAGGTTCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G ---		---	AAGATTACGGACCATAAGAACTGCCCTCCGACCCATACACACAAATTTATAGCAGGTAACCAAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAAAC/GJTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G ---		---	CCTCAACCATCTGTAAACCGAGCCGAGJAGJAGTGACCGGAGCTTGTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGGTCAGTCAGCAGGTG
EST14083 7	23 A G ---		---	CAATGGTGTCATGTGAACATATJAGJACCTATTATCAATAAGTTAAAAATAATCCCTTCTTGAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCACTCTGCTAAATGACCCGAACAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AAATCAATGCAATCTTGTGGCATGCTAGACAGAGGCATTAT/CJTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCTTCCACTCATTTTAAATGT
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATAJAGJAGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTGCCTTTTCTAACATTTTTCATATCATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCCAC ATACTGGTT	CGGGAACA GTACCGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCTCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGGCGGTATCACCCACCACTACTGGTTJATJTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---				TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTCAATCATATATAGCCAAAGGACTC/AJGGAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAAGACAA AGACAACAGA	GGATAGCTGA AACAGAGATA TTATTCTC		GTCACAGCACACTTTTATTAAGACGTGAAAAGACAAAAGACACAGAGGA/G/CJAGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGGCCAT GATAGTTGATG	TTCATTATTCC CTATAA		AAGGATTGAAAACATACCTAGATCATATAAAATTTGTGAAGGTTTTGCCATCACAAAGC/G/AJTTATAG GGAATTAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAATTTGCCCTCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	GGTGGGAGTCT CACTGTAAGG TC	CTTCTATCTTT CTGTTCTCTCCA		CTTCTTCTCTCTAGACGTGGAAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA/C/TJGATGGAGGAACAGAAAGATAGAAAGTTTGGGGT GCTGATGAAATTTGGGG
WI-16783	64 A G G	TOCTGAGATGT CTTTTACCTGA	CTGCTTGGTTC AATCTTATTA	G	AAAAATGTAAACCTTAGAGGTGGCTCTTTTGTGTCACTTTTCTGTGAGATGTCTTTTACCTGAG/A/GJ CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---				CAGGACTTAAGGTCAATTTTGCCTGGGAAGACTTTAACTAAAGGTCAGGGCAACATAGGA/T/CJTGTA CAGCACCACTCGGACCAGGAAGTGTGAAAATGCTCACACTAGCGTGCCCGAGCCCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---				GGTTTGAAGACGCAGCTTATCTCACCTGCCACTGGGATTCATTTTGTAGAGCTGTTTTGTACGCC TTTTCCAGAAAAGGCCGCTC/G/CJGGGTTTTCTGAACCCCTATATGGGCATTTTTAGAAT
EST16089 9	96 C T ---				CGTCTGAAGTTTTCTTTTATCAAGTCACATCAATCCCTCGGGCCCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/TJAAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---				ATCCAGCTGTGAAGGGACAGGAG/C/GJGTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---				TTCITTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCTCCAGGGA/JGJTTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---				ATGGTATAACAAAATCAGTTCAGGTTTTTTCTGGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAAACAACATAAAACACCCCTCTACGTCTAATCAGTCACTTAAGATA/T/CJCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---				ATGGTATAACAAAATCAGTTCAGGTTTTTTCTGGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTTAAACAACATAAAACACCCCTCTACGTCTAATCAGTCACTTAAGATAATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATCAAACGAACCTCTATCAAAACACACAAAGGCCCTAGAGGAGAGATTAC/TAATGAACGT AAATAATCAAGGCAATTTTGATCTAAAGCAATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGGAAGATAGTAGTGCAATAAAATGGTAAACAGCAG/G/AJAATGGAA TTATAGCTTCTTTTCATATAGGAATTGAAATTTATTTACTGAGGGTATAGGCAGAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACCTGTGGTTCACAGCTATTGTTCTTTCAATAAAGAAAGAAATATCTAGTTG/A/GJGTAG AGGAAGGCACCTGCTTCTGGCCCTTCTGTTTCATATTTTATGTCACTGTCTAAGCTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTCAAAATCA/G/ATACAGACAGATAAGAGCTTTAAGTATTTGCAATTT CCCCAGAGGAAAGTCAGCATCATAAACACATGGTCACATGCTCAGGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGT/C/CCCTGTGCAGCC CTTGCCAGTTTCCACAGGCGAGGATAGTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACAGGCGAGGATAGTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTCTCAGACCTCATGCTGCTGGAACCTGGTGCACATGTCATCTTGAACATATCATTTGGCAA AGGGAATGGGTATCAAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA/G/ACTGTGCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCACCTCTCCTGTGGCTTGTCTGCTGTCAGCTGCTGCCAGTGCCACA/G/JTGGTCTAGCCTCATGG CAGAAGCAATTTAGCCAACTGCTGCTGCTGCCACTCTCTCTCTTCCGCGCTGGGGCTCACCACC TCTTCTCCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAAGCTGG/G/A/JCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCCTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTCTG	CAGCTTCTGAC	GTCACCCAGCCCAATGCTTCAGGAATAATGATGGTGTGCTGCAGCTGTT/CJGTCTTATGAAGAAGTC AGAAGCTGATAAAGCTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAAC/T/C/GGAATAAGAGCATAAAACGGACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACACAAATAAGCAGCTAATGGCAATG/A/JTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATTTGTTTCTGATATGTGGAGAAATCTGCTCTTTATGTA



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WI-16879	79 C T	GATACAGGCC ATAATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATAATTTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATGCG	ACATGAATGGCAACCTCTAGGTGGGAGAGACAAATTCCTCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTGAC[AG/G]CGGATTTTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACITTTGG GCAGGTTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACCTTTGGGCGAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAAAGATATAGACA
WI-16910	74 G A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTCTTAAGGAGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACCTTATTTGGGCCIGAACCCAGTGAAAGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAACTACCACCATCTCTCTGCTACCACAGAGCAGTAAATCTAGGAATTTGAC TTTACTGCAGCCATTACACCAGCAC[C/T]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGOC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAGACTGCAATCAAGGGAAGCAGACCTGGGG[C/C]CCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA GTCATATT	CATTTGTTTTACTTTAAATGCACACTACATAACAACCTAATAT[C/C]TTAACTTGGTCCAACTATTT AGTATACTAATATGAGTTTTTATCTGATAACTTGCAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAGAGCAGTAGAGACTGAGGTAATAGTATTT[C]ACGGCTGG AAATCAACATGCCCTTCTCTGTGAAGTTGTGAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAGTACACTGTGTCGCCCTCATCTGAGAT[G/G]GTG TAGGACTGTAAAGGAATGTGTTGGGGTTTAGGAA
WI-16992a	46 G A T C	AAGCACCCAG AAGTACACTG C	CACATTCCTT ACAGTCTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAGTACACTGTG[C/A]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTGGGGTTTAGGAA

WI-17010	23 T C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTCJATGACATTTCAAACACCGTATTATTAGAAGCTCATTTAAT TGTTTAAATGCAGACAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74 C T	CACTCGGCAC AGACAGAGT	GGGAGGGCAGG GGTG	ATTCCGTCCTCCAAACAGGATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTCJTTGGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCCTAAGTAACAAC
WI-17040	94 T C A	AATCTCTTAT CACTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGGCTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAAATCTCTTATCATCTCAAGCCAGTCJCATCACTGAATAAGCCATAGTCCCAGTCTGTTTTCC AAATCTTCTCATATTGT
WI-17044	47 G T	GCAAGGGAT TAACGTATAG	GGGATCCOCT TGTTAAGA	TTGTTTGTGTTTTTCTCTCTCTGCCAAGGGATTAAAGTATAGGTCJTTCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCAGTCTCTCTGCAGAAATGGCAGGGAATCGAAT CAAAAAGAAAAGCAAGTG
WI-17021	62 T A	TGGACTTGTCA GCCTATAACT	TGTAGAGTTAG TGCCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTGACGCTATAACTACTCTJAJG CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCAGATGCCAAAAGTGCCTGG GAGGTGCCAATAAAATCAA
WI-17065	90 T C	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCTGTAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTTTCJAGGATTTCTGCTCTTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGT	GAGATGTTGAA AATGTTCTGGA A	TTCTAAGGTTGTACAGCCAACATCACTGTTTTCJATTCAGAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATTCCTGTAGTCTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G ---		---	TGCTGACTGTCAATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGGAT AACCTCTACACAGGCCTTJGCTACATAGGAGTATATTTGGCCAAAGACTACCAGTAGAAGTGATTT CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTTGATGCTTTGCGAGCTTCCCATTCATTCCA AATCAGAAAGCAGTCAGTGGCCCGGTGTTCCAGACGGCTTCJCTCTTTGTTAAGAAATTA
WI-17104b	108 T C ---		---	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTTTCJGCTCTTCACTCTGCTATTTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGTCTAAAGAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17114a	37 T C	TTTCCATCAAG GACTTTGTTTT	ATAGCAGAGTG AAGAGAC	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTCT TTCCCTCTTTJG/CATATCTCCAGGATTCCTGAGAAAGGCCCTCTTTGCTGCTCTAATTT
WI-17150	76 T G	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	GAAATCGAATACGTCCATTTCTTTGTAAAAATAACAATAAGTTTJGJAAGGCCAAAAGCAAGATTCTG TAAACCAACATTGGAAGGGGACACAGGGAGGGGCAGAGGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA
WI-17163	43 A G	CATTCTTTGT AAAAAACAAC	CAGAATCTTGC TTTTGCCCTT	

[illegible]

EST20824 8	115 T	AGTCGGAGT GCTGATTG	AAGATTTTATC TTGGACCGGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCCAAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT[G/G]TAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GIG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTATATAGCCATTTTAAATAAGTG[G/G]T TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGGTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTT[T/C]GTGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCTCTGCCA	ACCATGAAGG ATGCGGT	GTTTAAATGATCACTCACCACAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATATTCTGCT ATTCTGCCATT[C]ACCGCATCCTTCATGGTAGAGTATCACAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92 T C ---		---	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGTTTACTCTAT[C]GTCAAAGCTGGGCAAGTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G ---		---	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCC[C]G[C]CAGTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAAGTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATAT[C]ACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAAGTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C ---		---	TCGAGGAGCTCTGAGGAG[C]CACCAGGGAGCTGTGTCCAGGGCCACCCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCTTTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTTAAGTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCAGGTTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCAAGAGTTTACC[C]G[C]TGTGAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	GCATGAATTTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CAC[A]G[C]CATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCOC	TTGCCTGTAA TTTGACTGTAA TG	GCCTTTTATGTCTCTTTTAAACATCAAAATGTTTTATAACACACTTGATCTTTTGTCTACCCCA ATT/CJATTACAGTCAAAATTAACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGTGTACTTATATCTGTACAAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTAAATCTTTGCCTTT/AJATGGTTTTGACAGTTTGTGTCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAACATGCAAGTTTTCATTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAAATCTTAGGCAAAAGCCATTTCTTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17387	55 C G	CCTTTCAGAT TGAAGAAAAA	GCITTTGCCTA AGATTAATAGT AACTACT	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
EST23869 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
EST23733 9	31 T G	TTGTTTTGTT TT	TGCACITTTAA TCCCATCAAT	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17470	83 A G	GTCCCGTCCCG CCAG	CCAGTGACGAG GOOGA	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
EST25356 3b	95 C G	---	---	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
EST25356 3a	26 A C	---	---	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17581c	99 C T	---	---	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17581b	86 T C	ATTCAACATT ACTACCAAGTT CATTGATAA	CGTCAATGTAA ATTGCGCCT CAATCTATAG	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17596	86 A G C	ACTTCTTTGTG TAAACACTCC	CAATCTATAG CTAGAAATCGA CAATAT	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG AAAGGCTGTAGTTTGTGTTTTTGTGTTTTTCTTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA CTGACACGTCCTGTGTGCGGGGGTGCTCATGTGCGCTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTTCC

WI-17623	46 T C ---				TG TGG TTT AAT TTT AAT TCC CATA TAA TTA ATGG TGG GGCACAT T/CJGCATGTGCTTACTGGGTC ATT CATA TATCTTTGTGAAGCATCTGCTCCAA TCTTTGCCTGACTTTGGAGTTTTTTGGT
EST26419 1b	46 T C ---				ATTT CATA CAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA T/CJGGG CAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A A G	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGCC	ATTT CATA CAGAGATACAAAGGCAACTATGTGCAG C/AJAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ---				TCAGCTTTAATTTAAGGACATGTAATAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTGC TGTTCATCTTTCCATCTTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---				TACTTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTC/JGJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGCATGACGGGAAGCAGAG
EST27152 1	101 C T ---				CAAAGGATTTTATTTTGTCCCTAAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAAACATTTTCAATCATCTCTCTCTC/TJTTACATGGTGTACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 10a	33 G A ATT	GCACTTTGCAA CAATTTAATA		GCTGTGTGAT GCTACTGTAAT G	TTTTGCACTTTGCAACAATTTAATAATTTATC/GA/JAATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTTCAGTATTCTGTACACATTTCTGTTAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTTG C	CACATTCTGTT CTCCAGTCTTG C		TTATGGAATG GCTTATGTAAC C	ATCTTAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTGCT/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788 3	100 A G ---				ATTTTATTAGGCGGTACAAATCCAAAGGTGGTAAGGGTGAAGGAAAGGGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACCTTTACATTTCAAGGAC/JGJGCTTCCAGACAAGCCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC		GTGCAGAGAGG TACTCCAAGTA C	TCCTCTAAAACCTTCTCTGTTGGATCCCAAGTGACGTGGAAGTCATCAGAACCCCACTG/JA/GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAAATTC AATCTGTAC		TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/GA/JAAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---				TCCCGCTCCAAAAGCTTTATTGGCAATATGCTCTAT/CJAAAAGAAATGATCAATCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACCCGCTGTGAAGGAGACTGCTGTGTG TCCACCTCTTATCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT	TTTCTCGCATT TATTTTATAC CA	CATTGGAGTAAAGGTGTTCTTCTTTAAAT/AAATGGTATAAAATAAATGCGAGAAACATTAAC GGAGATGTACAGACACAGACGAAGACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGCTCC TGTG	TGGGTTGGCAG TGTC	AGAAITGGTCTAGTAATCGTTCAGGATTTGCGTGATGGCCCTCCCTGTCTGCGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGTCTATT/AAATGATACATACCAAGTGTACATACTG TTT/CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AAATCAITG	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGTCTATT/AAATGATACATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTTGTCACTG/AJGCTAACTCCT CAAATCAACATAACCTTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTTGAAGGACACCCAGCTTTGTTGGACTTAGGGCCTACCTATTCCAGCAGGTGCC/AJGTTATTT TCACCTGGTTACGTTCTGAAGGACCGTTTCCAAATGAGGTTACAGTACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTG TCATTTCTTG T	ATTATTAGTATCTGCTGTTGGGGTGGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/AAACAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATAATTAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTAAGTGGCTTCACTGATGAGGCAGTAACTACATAGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAATAATTCC/AJGJGATTTAATTTCTTCTAGTTCATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGAATCAAGAAGAAAGACCCAGA GTTTCAATAATAGGTAGC/GA/ATAACCCAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA	CTACCTATATT GTGAACCTTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGAATCAAGAAGAAAGAAAGTTACCCC AGAGTTTCAATAATAGGTAGCGATAACCCAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT	TGGGTATAGG AACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG/AJGJGCTGTTTCTTATACCCCAATATCATAAGAAAT GTTGTTGCTTCTATATGTTGAGCTTCAAAATTTCTTTGCTTAAATCAATCCAAATGAATTACCTGAAT TTCTCCTTGTGTTCAAAA



EST31951 4	87	C T	GGGTTGTCAG CCAACA	CCACCAAAAT CACTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTTGCCAGCCAAACAC/CTGGAGGTGATTTTGGTGGGAATCTTATCACAATATTCT
EST31968 8b	95	T G	---	---	CGAATTTGTCCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAAGTCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75	T C T	GGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAGTCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103	C T	---	---	TCATGGATGAACAGACGCTACATGCCACATCCCACTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGTCT/GTTCAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTCCAAAGCATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/AG JTCTGATTAGGGAGCACCCCAAGCCAGTAACAATATGGTCTTGACAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTC/GJAAGACTGGGATTAATTGTAGGAATATTTTCACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TGGCTTAGGT TCTACTTGATG T	AAACTGTCACTTCTAAAGTCTGGGATGACTTTCCT/GJATCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGTAAGTCCCAAGCTGAATTAATGTTTCACTCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATTTGCTATAAGGAAGGGGAACAAAATCTTTA TAGTGTCCTAAAGATAATTAATCTTGTTTAAATCTTTGCCAGCAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121	T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTTATAGCCTACTTCTCAAAATTTGT/AJTTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAACTACCA
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	GAAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCATGATC AATCGCCACGAGA/GJAAGTGGATGCCAAAGAGTATGG
EST33301 4c	80	G A	---	---	GAAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCATGATC AATCGCCACGAGA/GJAAGTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCAT/GJA ATCAATCGCCACGAGAGACTGATGCCAAAGAGTATGG
EST33460 1	44	G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTCAGCGGTGGTTTTCAATACTAAACA/GJATGTAACAATGCAANTATT TAACAATAAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAACTACTTTGCAA



WI-17904	50 A G A C A C	AAAGCATGAC AATAAAATGA	CGCTTATGTTA ATAGTAATTC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACATAAAATGAACACAG/GJTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACAAACAAATGA GTTTTTCTTTGAGTGACAAAGCTGTTCAITTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGGATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCTATGAAAAAAGCAGCTAGTTCCAGC TTACAAATCACACAAGT TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA	AACTACTAGGG AGAACAATA ATAAAATC	GGTACACAATTTTAAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGACCATATGATATACTCTTAAAGC/CJTJGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA CTCAGTAACTCCGGTGATATAATCTGCCATTTATTGATTTATGATAAAACACCTCTCATTTGTGA AAACACAGCTAAGGGTGACATCTCCAGACCCCAACCCTGCTGTATGTACJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCCAGGCCCTGCGAGT AGAGCGAAGGGAACAGAG/GJGCTGCCATGTGCTGTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGAGACCGGGT ATTCCTTTATAAAACACCATGTCCTTAAATGT/CJATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT GCCACTGAAAAAGGTGCTCTCCACJGCTTTCTAACTCCCTGACTCCCTCATTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACCTTAATCA TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCJAGJCTTGA GATTCAGAATCCAGAGGGTCTCAGTCTTGGTTAGGTGCTTCTGTGACATTTCTCTTG AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTTAG AGJACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCTGATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTT AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGTGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCTGATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTT CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAGJATGGAAGCAGGGTGAACG CATGCAAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTAGGTTGGTAGCAACAGAGGTAATG
WI-17982	98 C T C C T A A A G C	GGACCATATG ATATATACT	CAGAAATATG TGATAATACT CCTTCC	
WI-17993	118 A C ---	---	---	
WI-17996	84 A G A G G G A A C A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	
WI-17136	33 C G ---	---	---	
WI-18041	24 A C ---	---	---	
EST35164 8a	57 A G O O O C	CACAGCCCTGC O O O C	CCCTCTGGATT CTGAATCTCAA	
WI-18052b	67 A G ---	---	---	
WI-18052a	50 T C A T C	CCTGAGTTCCT TCATGTACGA	CTCAGGCAGCT CTGCTGT	
WI-18054	46 G A G A G T A A A A	GGGAGTGGGG G A G A G T A A A A	CGTCACCCCTGC TTCCA	

WI-18064	54 G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGGGGTAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGTATTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAACC TGCT	TTAGCACCACTTCTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C G T G T A T	AACCCACTAC TTACTCAGAGT	AAAACTAATA AGAAACTGGA	AAACCCACTACTTACTCAGAGTGTGTATTA/CJATATTAAACACATGAAAGATAATACTTAGAAAAA ACCTCAGTTTCTATTAGTTTGTATTTCTGTACTCAGAACGCAITTTAGGTTGCAAGGATATAA
WI-18080c	80 C T ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65 G A ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCC[G/ A]TGTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41 T C A G T C T C	GCAATATCA ATATCAAAC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTCTTTGTAAATTAATCTACTATGCC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63 G A ---		---	GTGGCATCCTATAAAGCAGCCCATGTGTTGAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTTACACGGTTTCTTCAAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGCTAGC TTAGGAGAGGTGTTTGAA
WI-18115b	71 C T ---		---	AACTACATAGTATGGTGCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T T T	TTAGTGACCT TTGGTATTCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G ---		---	TTTTGAGAAGCACTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTTTTA GGTAATTTG[C/J]TAAGAACAATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G G A G C T C	CCATCTTCCG	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTCGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTCAGGAGGAAAGGTGTATCCAGCAGCCATCTTTCCGGAAGCTC[G/J]GTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A ---		---	TGAAAGAGTCGACACAGCGGACACT[G/J]TCATAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62	G A ---	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG	---	TGAAAGAAAGTCGACACAGCGGACACTGTATAGTGGAAACAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAATGAGCTGGAGACATTAACTCTGGCGA
WI-18181	100	A C CAGATC	AGCAGAGTTG CTGCCCTC	CCTCCCTCTCT CCCC	---	GACAGTGAACAACATTGAAACACAAATACAACAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTGTTCTTGAAC ATTACATACAAGCATTTCTGAGTACAACACTAGGGGACAGGTATTTTCAAAAAACAATAGAGCAGA GTTCTGCCCTG[A/G]GTGTCGGGGGAGAGAGGGGATTTCAGCATTTTGGTGAGTATGTTAATT CCCTCAAGTTAATCTTTC
WI-18215	78	G A CTGCCCTC	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT	C	CATTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/G]GAA CCCTGAAACCTTTATTTTGAATTGAAGTTTTGCTCAGAACTGGGCGAGAACTTTTCACATTCTG AC
WI-18232	60	T A A A	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT	---	TTTAAAAATGCTTAGATTTTCCCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C/T]GTCTCACTAGTCTATTCACCTCTGTGGGCATTTTCGGCAGAGTGGC
WI-17892	76	T C A C A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	---	AATATCCCCAAATGTTAATCGTAACATAC[T/GA]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG
WI-18242	30	G A AATCGTAACA	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266c	119	C T ---	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C ---	AAATAGGAAA TATGGACTATC	TTTCATGCATCA TTTGTGCA	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T T TCAAA	GGTGTGAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	---	CTGAGCCTCTTGGATATGTGGTTAGTGTCTATCATTAAATTTGGAAAGCTGCAGCTATTGTTATTC AAAT[AGTATCTTCTGCTCCCTTTCTCTCTTTCTGGGATTCTCATTCTGCATGTGTTATA
WI-18312	73	A G A A	---	---	---	AAACATCTACAGCTGTCTTAGGCCATCTCTGTAAAGAAATCAGGGATAAGAGCTGAGGAAACAAGAGG A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAATAAGAACATAATTTTTTTGTTGAT TCACA
WI-18330b	66	A G ---	---	---	---	---

WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGATAAGA/G/AJCTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAGAACATAATTTTTTGTGGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAACTACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT/CJCTCATTTAGGGCCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAACAATGGTGAACACAGCTTTCGTTAGGCTAGTT/G/AJGCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAAATACGAACAGTGACGCTGATGG CCTGCAGTCCCTGCGGTGCTTGGCTCTCTGGACG/G/AJTTCATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAAATACGAACAGTGCA/C/TJGCTGA TGGCTGCAGTCCCTGCGGTGCTTGGCTCTCTGGACGGTTCATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
WI-18357	89	C G G C A T C A A	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTGTGAGGTGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA/C/GJTCATCTTCAGTCTTTGAGTCTCCAGCCAGGTCCAAAGCTT GTGGACACAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGGTGAGCTCCCTTCTTAATGGCCTGAAGGTCACTCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTTCG/G/AJTGAAAGTGTTCCTGTATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGGTGAGCTCCCTTCTTAATGGCCTGAAGGTCACTCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTTCG/G/AJTGAAAGTGTTCCTGTATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTG C C C T T	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTGAGCTCCCTTCTTAATGGCCTGAAGGTCACTCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTTCG/G/AJTGAAAGTGTTCCTGTATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGGTGAGCTCCCTTCTTAATGGCCTGAAGGTCACTCTCCTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTTCG/GAAAGTGTTCCTGTATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCA TTGT/GA/JATTAAGTTTATTAAATCAGCTGACTTTAGCA TTGGGAGATTATCTGGAT

EST38512	91 T G	TGACGATGCG	CACTGCACTCT	TAATAAAAGTACCCCAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAT
7		AATACTTCG	GGGAAGC	ACCTGATGACGATGCCAATACCTCGT[G]GCTTCCCAGAGTGCGAGTGATGAACCTGTTATAGCC
EST38519	24 C T T	CCTGCACTCC	TCTGTTAGGAC	CCTGCACTCTCTAAAGATCTTTT[C]TTCGCCCAAGTCTCAACAGATGGTATATTCCTCTGGAATA
0		TAAAAGATCT	TTGGGGA	AGATGAACGTCATCAATGGATTGCTGCTCTCGTTTCAGCTTTGATTTTTTTGCTCTGAGAACCTTG
EST38575	68 T C A A	GAACATCCCA	AGGGAAGGTA	TCCTCCCTGCTGATTT
1		TGTTCTGTTT	GTATAACACAT	AGTGGTCAAAATGTAATACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTCTGTTTAA
EST38616	101 C G C T T C	CCTGCTC3GC	AAGAGA	T/CJTCTCTTATGTGTTATACTACCTTCCCTTCTCTTCTTCTTATACACATAGATTTTCCCTAAATTCAGC
9		C T T C	GAGGAATGAT	CCA
EST38652	59 T C C A T T T C A A	AATGGTCATTT	GGTGC	CCATCTAGGCAAGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTCAGCCCGGGGCCCCGGTGG
8		CA T T T C A A	AAAGGAAAA	AGTCTCGGGGGCCCCCGCTCGCCCTTCG/GGCCACCATCCATTCCTCAGGGG
EST38654	42 T C G T T T A C A	TAATATATCA	CAGTGATGGTC	TATAGTAGGTACTTTCTGCTGCAGCAGGAATATTACGTCTGAACCTGGGCAATTCAA[T/C]GCGTG
5		G T T T A C A	CTTAATCTTCT	GTATTTTTTCTTTTCATTTTTGCAAGTAAAAAATCAT
EST38707	75 A G ---		ATC	CTCAAGCTGAGATGGTCATTTTAAATATATCAGTTTTACATAT[C]AGATAGAAGATTAAAGGACCAT
9			---	CACGTGAGTGCATAGCTCAGAGGAGGATTAAGATTGGACCCAGGAGGTGGTTCCAGCATATA
EST38759	86 A G G T G A T A G G	TGTCCTCCTGA	TCACCATCGTG	GGATCCTCACTCACTCGGACAGCCTGAGAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA
2		GGTGATATGG	GACTTAAGG	CGTCCC[C]GJAGGCCAGCGGGATGTGTGCCCTCTCTCTCCCAACTCATCTTTCAGGAACACGAGG
EST38775	40 T A C	AATCAATAGG	GGCTTTGCTCT	ATCTTGCTTCTGGAAA
1		AGAGGATTGG	GAATTCAAA	TGACCTGTTGATTTCTTCACTAGAGGGGAGAAATCACTACCTACCTTTTGGATGCCCTCCCACTCTACTTGT
EST38815	91 C A C A	TGTTATGAGA	GCTGACTGGCA	CTCCCTGAGGTGATAG[G]GCTTAAAGTCCAGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC
4		ACCCATTACA	CATGCTTT	TAGCAGCACG
EST38858	98 C T T G A C	CACGAGTAAA	GGAGCGAGTCC	GACTCTCAACCAAGAGAAAATCAATAGGAGAGGATTGGCT[A]TGTGAATTCAGAGCAAGCCCT
4		AAGAACTCA	AAGGAGAA	CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCTAAGTGGTAC
EST38865	72 T C T G T G C A T G C	GCTGTAGAATT	GGAAGGACGG	AAACAAACCAACATGGTGG
2		TGTTGATGC	AGGACACAG	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTCAATTCACAAG
				TGTTTATGAGAACCCATTACACA[C]A/AAGAGCATGTGCCAGTCAGCAGATTCTGTATAATA
				TCTTTACTGTGCTTACAACCTTTCTCCAAAGTTTGGGTGGTTCCATATTGTTATTGTTATTGTTATTA
				TTCACACGAGTAAAAAGAAACTCATGAC[C]TTCCTCTTGAGCTCGCTCCTCTCCCCAATCTCGAT
				ACCGACTGCACGTGTG
				CCTTAATGGATTTACAGTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG
				ATGCT[C]CTGTGTCCTCGTCTTCCCAAAATGAGCACATATGCGGGCAGGCAAGCATGCTGGA
				TTTGCTTAGTTGTTAA

EST38878 9	47 T	AAACATCATT ACTAGCCTAG C ATCCTAA	CCTCAATAAA TCTCATGTCTT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCCC TTATCAATGTCTCATCTCACACATCTTTATTTTATTTTGTCTCAATTTCTCAAAATCGGATTTGTC TCATGAGAAATAATGGCTGAGGAGCTGGCAGCGAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATCAATGTCTCATCTCACACATCTTTATTTTATTTTAT/CJTGTGTTTTCATTTCTCAAAATATCGGATTTGT TGCTCATGAGAAATAATGGCTGAGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	
EST38909 5	47 A G	GCACAGCATG GCTAAACG	GGTATTTGTG ATCCCATCTT T	GCACTAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAAACG/A/GJTAAGATGGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G C A C	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACAACTACACATCAAACTTAGGGAATGTGGTTAGTGTGTGACGTTGAG GGAAACTTATAACCTCAC/A/GJGCTTGTTCACAAAACACAGCAGACACAGAGATTTCCCACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C G G T G G G	TGAATTCCTT GGTGG	CACGTGCAATCT CAOCC	TAAACATTCCTTGAATTCCTTGTGGG/GC/GJGGGGGGGTGAGATTGCAGTGTCAAGATAAA TATCACAATATATCAAACTTCAAAATGTGTATGCAATTCACACACTGACATGAGCCACAACAT CCTTTCACAGGACTGTAC
EST39002 0	42 G A T G A C C	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGAGATCCCGGACCTTCGGTGAACG/A/CAGGCTCCCTGCCAGGGCTGG CCCTGAOCGGGCTCCCGAGCTCGGCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G C C T A A G G A A T	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG GGC	CACGTGGCCCTAAGTTTCCGGGTCTTCTCAGTCTGGATGGCTGTGTGGAAGGCTTGGTGGTAAG GCCTAAGGAAT/GJAGGGGCGAGGGGGCGATGCCGCCAGCGAGATGGTCTGTAAAGCCTGTGGGTC AAGACCTAACTTCTGGA
WI-16398	90 T C T C A	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTATCACAACGCAACATATAGAAACATAAAAGAAATAAAGTATCCACCCTAAAAT CCCTATTATTCATGATATTTTCA/T/CJAGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C A C T	CCTTGTCTC AATTTTAAAC ACT	TAAGGGTAAT TCCCTATATAA AAAG	GGTTGTCTTTCATGTATTTTCTCATTTCTCATCAGGTTTCTGGTCTTTGTCTCAATTTTAAACAT T/CJCTTTTATATAGGGAATAGCCCTTAACTGTGTGATACATGCTGCCAAAATTTCTCCAGTT
WI-16406	24 C T A G G	GCITTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAA AA	GCITTAATGGCTACAGAAAGAGG/C/JGGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G G C T	TCATCTGAGA ATAAACTTCTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTATGATTGTTTCATCTGAGAAATAAATCTCCTGCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T G G A T G C C	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATTGCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTACCCACAGCC AGCTCTGCTTGCTGTCAT
EST39366 2	72 T C ---		---	AGAAACATCTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGTTCAGA
EST39371 9	86 A G G G T G A G A G G T T	CATTGGATTA GGTGAGG	TGATTTGAGAC ATTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAAGTTTATTTATGTGTGTAATTCACAGTTGAGCAATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAAATCAATGCTTCTCTTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G ---		---	ACAAGTGACATATCCAAACCAAC[C/J]GCCATCCCACTGTGCCCTATTCCTTCTTGTTCTTT AGAGCCTTTTACAGCTATTTCTGTGTAAGCAAACTGCACGAAGGCCCTCCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T A T T T G A T T	GCTCCCCACA TACTGATGTT	GGTCCCTTATG AAGCCACC	AGGTTCTGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCGCTATT TTCTGGTGGGCTAGGTAATTCCTGTGCTTGGTCCACAGAGACAAATTAAGAAGATCAGGTCT GGCTGTGC
EST39430 2	45 A C C	GGCAGAGGAA TACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T G A G T A A	CTACTGACAT AGGACTTCA	TCCTGGAAAAC TGACATAAACCC	AAAGCCCTGTAAACTGAAGCTAGACAAGTCAACTTTGGAAGAAAATAACAGGAACCTATTTATAT ACGTAATACACTTTTACATACCTGCCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCCC
EST39465 2	80 A G G G T G C	AATGCAGGAG GGTGC	CAATCTGGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGTGG[C/A/G]AGAGGGGCCGAGATTGGGTGTTCCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G A C A T T A G	AAAGATTCTT GTAGACATCT	CACITGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGACAGACTTCTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C ---		---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTTGGTGACCCCATACATTTTGTGTC CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAGA



WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAGCATG TGACCACAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACIAGITTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAGTGTATGTGCGGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGGAACTT GAAACAC	TTCTTGAAGA AAGGCGTC	TCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGGTGGA ACCTGAAACACIAGIACGCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT AGGT	GCACACCTTC ACACTGTTA	TCATTCAGTGTATCACATCTTCAGGATAGGTIAGIATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGGA CA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTATTTTGGACACI/TGTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTACAAATTTCTCATCTACTGTAAATTTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATTCACG ATTGCTATAAG C	AGAGAGACAAACAAAGAATAAGGGGAAATGGGAAGAACACAGAGTGAATTAAGCAAATCTTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAAATCAAAI/CIGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTG TTTAATTTAC TC	AGAGAGACAAACAAAGAATAAGGGGAAATGGGAAGAACI/TJAGAGTGAATTAAGCAAATCTT GGATTACAGATTCCATTAAACAGGAAGTTTCTCAAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATTTC A	---	AGCTGATCAGCTGTCTTACTGTGTTTATGTGTGGCCAGGGGAGCCAAAGATCAGACACCTGTG CTAGACAGATTCAI/CJTGACACAAACACAGGAGGTGGGGTACACGGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CACCTGTCT AGACAGATTTC A	CCTCTGTGT TGTTGCA	AGCTGATCAGCTGTCTTACTGTGTTTATGTGTGGCCAGGGGAGCCAAAGATCAGACACCTGTG CTAGACAGATTCAI/CJTGACACAAACACAGGAGGTGGGGTACACGGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTGGCTCT AAGTGGGACT T	CTCCCTGACT GTATCCAGA	AAATTGAGGTCGGGTGGAACTATAAAAGGAAAGGAAAGAGAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCTCCAGTTCTTTTGGCTCTAAGTGGGACTA/CJTTC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCTGATGTGTGTTTGTGCACATTGGGGGCCACAGT/CJAAATAGGCTAAA AGGCAGTCCCACTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA G	TTTAGGCTTTG AGATGGTTCT	GGTGCTATAGCTGCTTGTACACCACAAATGGCAGAGGTGA/GJTAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGTCTAATCTCGGGTTTAGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGAGGGGTGGGGCCGGCTGAGGGTGGGGGTGCGAGG/CJTGGT CACTCCCATGTGCCCCCTGGCCGTCCCTCCACTCAACCCACACCTGGGCCAGTCCACGTTGAGGT



WI-18491	109	G A	A C A A A T G G T A G G T G G T A T T	C G T G T G C A T T T T C T T G T A A T C C	C T A A T G A G A T G A A T A C A T G G A G G G T T T A G C A C A G T G C C T A A A A C A C A G T A A G T A A C C A A C A A A T G G T A G G T G G T A T T A A T A C T A T T A T T A T T A A T C C C A G A A T G A C [G/A] G G A T T A C A A G A A A A T G C A C A
EST50757	79	C T	G A G C T C G A G G C T G C T T C T	A C C C T T C A C C C G C C C	A G C C C C C T C C A C T C T G C T T C C A C A A A G T C G G C T C C C G A G A G C T C G A G C T G C T C T C T T T T A T A T G T G C A G G G C C [C/T] G G G C G G G T G A G G G T C A G A G A
WI-17675	103	T C	G G A C A T T T G G A T G G T G A C T T	G G G G A C C A C C C A G G	G A T C T T G G A A A G C A C T A G A A A C T A A A C A T C T T C A C C A G G T G C T G A A G A A A G T G T C T C G T T T A A T T G C C A A G C A G G G A T G T G G A C A T T T G G A T G G T G A C T T T [C/T] C C T G G T G G T T C C C C A T A G A T T C A C C A T T G C C T C T A A T G G T G T C T A
WI-16543	67	G T	A G A T A A A C T A C A T T T G G G T T	G A T T C A T C A T T A C A G G G A C T T	G A T C C A T T A C C T A G G T A A A A T T C T C T G A A T G T C A A A C A A A G A G A T A A A C T A C A T T T G G G T T T T G G G T T A A G T C C C C T G T A A T G A T G A A T C A A G A A T C C T C A A G T C T G T C T T G C C A C C C A T T T A A T A C G T A T T T T T G T T A A G G C T G A A G T T
WI-17687	107	C G	G C C A A A A A G G T T G G G G A A	T T A C T T T T G T A C C G A C C A G C A	A T C T G A G A T G G A A G A G T T T C A T C C C A A A C C A C T C T C C C C T G A C C C C A G T C C A T G G A A A A A T T G T C T T C C A C A A A A C C G T C C C T G T G T G C C A A A A A G T T G G G A A [C/G] T G C T G G T G C G T A C A A A A G T A A T T G
WI-17690b	79	A G	A G G C A T T T T T C T A G C T G T G T T	--- C A A G A G T T A T G	A C A A C A T G T G A A A G A A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T C T A G C T G T T T G A T T G G C T C C C T A T A G A T T C A G G A C C C A A A C T C T T G T T C T A C T A C T G C T A T C T G C T A T G C T G
WI-17690a	63	G A	G C G G A A G A C A G T G A C T G T	G G T C C T G A A T C A T C C A G C T C	A C A A C A T G T G A A A G A A G A T A T G T C T T A C T C A C A G T G G A G G C A T T T T C T A G C T G T G T T [G/A] T T T G G C T T C C C T A T A G A T T C A G G A C C C A A A C T C T T G T T C T A C T A C T G C T A T G C T A T G C T G C T G G A T C C A A T C T C A G T G T C T A A C T A C A T C A T C C C A G A T T A T T C T G A A G T G G A A C C A C C C T C C G A C C C A A T G G C A A C A T C A C C C A C T A C C T G G T T T C T G G G A G A G C G C G G A A G A C A G T G A G C T G T T [C/T] G A G C T G G A T T A T T G C C T C A A A
EST51717	128	C T	T G G T C A C T T T G T G G C C	G G C T C T G C C C A C C C C	G A T C C A A T C T C A G T G T C T A A C T A C A T C A T C C C A G A T T A T T [C/T] T G A A G T G G A A C C A C C C T C C G A C C C C A A T G G C A A C A T C A C C C A C T A C C T G G T T T C T G G G A G A G G C A G G C G G A A G A C A G T G A G C T G T T C G A G C T G G A T T A T T G C C T C A A A
EST53012	97	C T	T G G T C A C T T T G T G G C C	G G C T C T G C C C A C C C C	T T T C C A G G T T G A C A G G T T T A T T C A C C C C C T T C C A T C C C C A T G G C C A C C C A G G C A G G A G A C A G G T G T G C T G G A G T C T G G T C A C T T T G G G G C C [C/T] G G C G T G G C A G A G C C C A C T G G G T T A C A T T C T G T G G G C A G G T G T G G A C A C
EST53349	96	A G	T G T T G A A A G C A G T C A C A A T G	C A T C T G G A T A T C T T G T C A C A T T	A A A C T G C A A A T A C A A A A A A C A G A A G T C C A A G A A G G C T A A A G T C T A A G C T A T A A T T A C A C A T G A A G T A T A T G T T G A A A G C A G T C A C A A T G T A C [A/G] A A A A T G T G A C A A G A T A T C C A G A T G T T A A T T T C G A A A T G T C C C A T G A C T T G A C A G A C T G A G A G C C A G C C A G C C A G C C A G G A G A C C T G C A G A A C T T A A A C A C [A/G] A G A C A T T A T T G T T A G A A A G G C A A G T C T T A C A C T G A A A T A G G T T T T A A C A T G A A C A C A T T A A A G G G A G A T G G C C
EST53389	74	A G	G G A C C T G C A G A A C T T A A A	G C C C T T T C T A A C A A T A A A T G C T	

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[illegible]

TIGR- A003P30	117 C G ---			ACAAGTTCAAAGGAGAACCTTCCTTTGTTTAAATGCAGCTGTGCTCAGAGCCTGTGATTTCCTAGGA AACCATCTGGGTTTAGCCCAATTAGAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A			GCTTGCTTTTATGTTAGTTTCGGGGGAAAGGGCTGACAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGTTTCAGAACTTCTTGCTTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATTCTCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGATCAGGAAGTACAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTGTCATGGCGATT[C/G]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTACAGGAAGTAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGTCATGGCGATTAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCT			CCTACAATCCTATAATATTGCAAGGGTGGGAAGGATGCAGGAACAGGCATTCTCTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACTTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAATTTCAAA
TIGR- A004V26	125 A G ---			TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAAATATCCAGAATAATTTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[G/A]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC			CCAGGCTATAATGTTGTGGTGGATCT[C/G]GCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCAACCCGCCACCTAACTAAATTTTG TATTTTATAGTAGAGACATTGTATTTTATAGTAGACAGG
TIGR- A004X20	25 T C GA			TAAGTTTTCCTTCTCTCTGTAGGAT[C/G]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT TCACTCTGGCTTCGCTTCAGAGGAGTTGATATTTTGAAGTGGTACCTTTGTTCTGTGTCTTTTCA GACCAACCGCTTCCTTCAATTTCTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCTT
TIGR- A004X30	26 T C CCAC			TTTTGAAATCTTAGAGTAGAACCCACT[C/G]ACTCTAGTAATACTTGTATAAATAAATAGTTT AAACACTTCCATAAAGAATTAGGGTGCCCGCTCTGATTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAACT			CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[C/G]TTGCTTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTCATATATCAATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAGTTATTGGAGGAGCTTGACACCCCTTCTGCGCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTCCCGATGACCATCTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCG GTDC	GTCTTAGCAGAGGAGATAAATTTGAGGGACAGCCCCAACGGCGCCAGGTAGCCTTCAGGGGGGGCA GGGTGGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTC/GTCTAGATTCCTTGGCCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTC/GTCTAGATTCCTTGGCCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTTACAC	TTGCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACAAATTTGGTCACTCACTGAACCTTGGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACCTGTACACTG/GTCTTGGCTTAAATAATAGACAATGATTTTGG TCTATTACTTAGTATAGACAAAGTGATTTGTTAGACAAAGTGATTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAAATTTATAACCCAGGCCTTG/AJCTACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCTGCCATGTGGATAGTACTCTTGGCTGCTTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAACTTTGTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAATGACCCCTTGGCTCTTTATTTTCTTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGGATGCTCTTCTATTG/C/GGATGCTCTTCTATTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGTTACTGCACCTTACAGAG/A/GJCTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTTATTTAAGAGATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGCTAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/A/GTACATTACCTCACAGCCAGGGTTGGCAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGCTCTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATCCCCCAAGAGCGCATATGAATCTGCGC

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X57830	106	GC CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGCATATCTGCTGATGCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTC
X74070b	72	TG TGGATC	CTTTTAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCT/GGATATAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTGTGCTTATACAAATTCATCTTTCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	CT ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAGCTTJAGAGCTTCTTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G ---		---	ATGACCAAAGCCACCACATTTAGAACTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTTTGTATTGACTGCATGAATGCGA GTTGTGCGTGCAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ---		---	CCACTCCATCCTGATGCCCAAGTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G ---		---	CCACTCCATCCTGATGCCCAAGTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	GA ---		---	CTCCCTGCCTCCTCCTCCTGCTGTGATGCTCGCTCAAAACAGCCGAAACCTGCTTGAATGGGGG GAGGGGCGGTTTC(G/A)CTTTCCTTCTTCTGGCTTCTCTTATCTTCGACAAACCAATCTCAATAAA GCCAAAATCTTCTCTTCTCCTCCTCAGGCCACCTCCTGCTCCTCACTCCTGCTGCTGGCTTTT CTGGA
D37931	64	T C ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT/CJ CCCAGGCTGTCTCCTCAGCTCATTTCTACTCTTTTCTCTATATAACTCATTTCTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101	C T ---				CAGGAGGACTTCAGTGTGATCCCTGCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCTGTTCCAC/C/TAAGAGGAGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCTGTTCTCTCCCGCTGGCTCTCGGTCTGGGAGGGTGACCTGTCCAGATGAC TGGGAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACCTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTCCCTGTCCTCCCTCCACCTTCCCTCAGATGTG TCTGGTG
D90145	21	T C ---				ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAGTACTTCTTATTATGAGCCCT/C/JGAGGA CCAGACATGTTATTATCAAGCCCTTATATACCATCTAAT
EST14035 1a	59	T C ---				GCATTTAAAAATTCACATTTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG/C/JTGTAGATTTTCAGATGTAGGTGCTCAATCTGAGCACTTAICT
EST16668 5	71	C T ---				ACAGACTATCGCCAACTTAAATGCTTAACTTTTATGATCAATAGTAATAATTACA/C/JGAGATA TTCACACTTTATTATAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT
EST16904 7	57	C T ---				TTTTTAAGTACCAGAGGCACCTGCTGGAACAGGATGAAAAGTATACAC/C/JGTTACTACTTACTC TTCACCTTTCAACCTGATTTCCCTTAAAGACTTCTACTTAGCAA
EST21863 9	49	A G ---				GGCTGAAGTAGAATCAAGGTTAAGAACATTTTATGCCTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGAG/C/JTGTGACAGTGTGAGCAAAAACACAA
EST21885 6	80	G A ---				ATTTAGTGCAATGACAAAGCCCA/C/JGAGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACAAAGTATGGGAGT
EST22623 8a	26	A G ---				AAAATGATTGAATTCAGGAAGTACATTTATGATCTCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG/C/JAAATGTGGAAAAGATGGCTTTTAAACCC
EST22644 2	98	A G ---				CCTCATTATTTAAAAAGACGGACATAAAAA/C/JATACACAAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST23587 1	31	T A ---				AAAGATCTGGCATTATTCACATCATTCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGTCACAGCATTTTAACTATCATTTTAGCGTAAATACCT/C/JGAATAACCATAGTTACAGAAATTGG GTCTGTGTAAACCTCAAT
EST24246 7	106	T C ---				TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/C/JGATTTAAAAATGTATCAAT GCACCTTCTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24308 3	45	A G ---				CTTGAACCTTCGGTCTCAAGTGGTACGTCCTCAACCTCCCAAAATGATGGGATTACAGGCATAAG CAGCG/C/JTGCCTGACCCACATTTCTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73	G A ---				TATTGTTGCATTATCAAAATGGTTA/C/JAGTTTTCAATTAACCTGTAATTGATTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAATCGTTAGTTAATGCTACATT
EST25089 6	25	T C ---				



EST25476 9	33 GA ---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAACCAACACACA AGAGGTCCTCTGCTGCTTTCCACTGAGCTGTGGCGCTGTGGACTTGGACCTGGCTGCTGA
EST26183 2	70 TA ---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAGATTGATCTCTAAATAAG ATT[A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 TC ---	---	AGAAATAAGGTGCTACAGAACTCATGTCGATAGCGCTTTCTTTAGGCACATATTATAGCAAT CAGATGAAAGTTCTGTAATCACACACACACTGTGCCCTTAACAACAACACCGGTGACTCTGA
EST27816 5a	26 TC ---	---	CAACTCAAGGTACAAGACAATTGCATT[C/T]AACATTGTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 AT ---	---	GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGAGGCGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 AC ---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACCTGCATACCTAATTCTTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAACAAGACAGACTCATTTCCTTTGA G
EST30935 9a	59 CG ---	---	AGCTATGGTAGAGCAAAATTCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAG[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTGTGAGG
EST32515 7	25 GA ---	---	CCGAATATAAGGAAATAATGGTGG[C/G]ATGCCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCTCTATGAATACTGGCACTGTTTATTCATGTTTATATGTGAGTTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4	27 TC ---	---	TGCTTTGTTCCCTCCAAATCCTAAA[T/C]GTGTGTCTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTTGACCATATTCAAGTATCTTGAATACAGGTTTCAGATACTATGGAGATGATACCATTT GGACTAGGTA
EST33352 7b	75 CG ---	---	TACACATTATCAAGAGACCACTGACATGCATCTCCTCCGCAATACATTCGTCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 AC ---	---	ATTTTCCCACAGCAGATATTTATGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTCAAAAAGATTTACAAATCTCAGTCATTACACACTGAGGCAAC[C/G]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 AG ---	---	CCTTTGGGGAGTTTAAAGCCAGATGTGACAAAGTCACTTACAGGAAGACTGGAAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCCATACTAAGCT GCTC
EST33508 1b	45 CT ---	---	AAAAACATGCTATTGAACAACTTTTTTATAAGAAATAAGTTGA[C/T]TGAAGAGCAGTTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA



EST33508 1a	36 A G ---			AAAAACATGCTATTGAACAAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGTTTGAATAATATGTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA[C/G]TCTTTGAACTACAGCCTGAATCCCC
EST34739 3	97 T A ---			GAAGTATCCTCCAGTGGCAGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACTC[T/A]GGTGCCTTACAACCTCAACTACTGCAGAAATTTCT TGTTGCGCTCATAAACA
EST34792 6b				ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTG[A/G]GTATTCAGGAATCTTAGTCTCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	104 A G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG[A/T]GCTTTCTGGTGGCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			CTTTTCAAATTTTTGATAGGCATTTAATG[C/T]TATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTTCCATTTTACTTAGTTGAGAACATTTTCAATTTTCATCT
EST35708 9	32 C T ---			CTGCCCAAAATTAACTTTAGGCAATGGAA[C/T]JAGACTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGTTGGCACTTCTCTGTTG
EST35747 9	51 C G ---			ATGTCAAAGTGTGGCT ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGAGTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATAAACTGAGGGAACAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCTCCCATGAACCAAG[A/C]TGTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---			CACCTGTTTCATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTTACCAAGTGTGCTAGCCTACAGC AGTCAGGAGGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCAAGACATGACTACCAACG[C/G]TGGCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTGT CACAGGGGTCTTAGTGT

EST36620 6	50 G A ---	---	---	GACITATTAGATAAGGGTTTCGGCTACCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAAGG AAGGCTTATTTAAATATGGGAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690 0a	89 C G ---	---	---	CCTGTGATGTGCATGGGTGCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCCTA/C/GJAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	---	GAGACAGAAGCCATCAGTTAAATGAGGTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACITTAGCTACCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	---	ACTGTCTGCCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/TT]CTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	---	ATGATCGCTTATGTAATTTGAGGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	---	GGTCTACTCTCTGCCAGGACGGTTTGAAACTCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTCTAGGATTACAGG[C/G]GTGAGCCACACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	---	AATAGTCTATGGCTACGGGCCCCGGGATGTTAAAAATGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTGAAAGT[C/T]G/CAGGAGAAAAATGGGGTCC
EST37284 2	93 G T ---	---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGGAA GCTCTCTGGATAATGTCACTCTAGGA[G/TT]AGTAAACAGGTTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCCTGAGGAATA
EST37315 2a	90 A G ---	---	---	AGATGGGCTTCTGTAGCTTGTCTCGGGCTGAACCTAAGATATCTCTCTGCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCTCAAACTT[C/TT]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCTTCACATAGCCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAAATAGATTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTCTGTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAAATAGTAGT[C/TT]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTCTGTCTCTCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63	T G	---	---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCTGTGAAAAAC[7G JAACATGCCCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAACACGTGTGCTGACATGATTAGCTT
EST37452 4	46	G A	---	---	---	AAGACATAAATCTGCAATGAATCAGTTATGAATATTAACCTCT[7G]A[7CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCAATTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34	A G	---	---	---	CTAGGCATGGGGCTTTACAGTCAATTTATTTACCA[7G]GTCATGAATTCATTAAAAACACACGGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAAATCACCCCTGGTTTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTTACATGTTTATATCACTTAT[7G]TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57	C T	---	---	---	TCTACCAGGTACCAAAGTATCTGTATATGCTTTAAGTGGCATTTCATGTCACCTTA[7C]TCGCATGG AAGAACGCTCTCCTTTAATTCCTTAACCTCTCTCTCTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100	T C	---	---	---	TAATCAAGGCCCTCTTTTCATTACCAAAAAACAAAAAAGGGAAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCCTGACTGAQ[7C]GTCCCTGCAGTGCCCATGGGTCCCGTGCT TATTCATTCTCCTCTCTCA
EST38950 5	25	T C	---	---	---	TTTATTTGCAAAAGTAAGCAGCCGGT[7C]GTGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCTG CTGGAAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90	T C	---	---	---	TTTTTGTTACTCTGTAGCCAGTCATTAACTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[7C]AAACAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70	G C	---	---	---	TCCTTCTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGGAAGACCAGCCATGGAAGGAAAGTA TG[7C]G[7G]TTTAGGGAGAGCTGGCAGCTGGCCTCTAACTCTCCCTGTCATTTGACACAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---	---	---	GTCACCATTGACCTTACATAGTGCCTCTAGT[7C]A[7C]TATGAGGCACTAGAACCTTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAATTT
EST40548 4	37	T C	---	---	---	TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTCT[7C]TCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAAGGCTCAAGGTGTC AATAATCTGTGGGACTCA
EST40549 1	42	A G	---	---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[7G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACACCATTTCTCACTTTGAACCTAGCTCCCTGCAAGCACCTTCTA CCCTGCACTTTGGGGAG
EST40579 1	81	A C	---	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCACTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[7C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68	A G	---	---	---	TTGTATGGTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTATGACACACCC A[7G]TCTGTACTCCACAATATCCTATGTTTAAAGCT

EST51340	51	G A ---	---		GATCAAACTGTATTGCCAGGCCAGCTCCTCGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134	T C ---	---		CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGGAGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAGT AGCTG
K01506	63	T C ---	---		CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTCTCTCAGCTTCTCTCAGTGAACACTACIT/CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCTCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69	T C ---	---		TGAGTCTGAGCAGCAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAAGGOC CT/CJATCCATTAGTTCCACTGCTCTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTCTGTCTATTGGATGACITTGAGATTATCTTTGTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36	T C ---	---		GCATTTTACATATCCCAAGCCCTTAGGGCTACAGT/CJCTCTTGTCTGACCCCTGTAGGGTGCCA TTTGAGTTTACAGCCTAGAAGAAAGAAAGGCTTTGGGCTGTGTGTGGCATAGGCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTGAGACAAACCTGGGCAAT GT
L38517	137	G C ---	---		GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCTGCCATCTCCTCTGCCATGAAGATACACCAATTGAGACTTGACTGGGCAACACCAAGCGTCCCCCAG CQ/CJCGTGTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123	T G ---	---		ACTTGAGAAGCAGAGCTGGCCACCTTCTGGAGGCCACTGTGATGATGAGCCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTAGTTCTTTTGTATTTTGTATATT/GJCGCCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCGGTGGGCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173	G A ---	---		CAAAGTTGTCTCTGCCCATGAGCACACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAAACAGC CCTGTCTCAAAACTGGGTGCCAGGTCCAATGTACCAGAGCTGGAATCTGAAGCCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCTACACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 TC ---	---	AAGTGAACAGAAAGCAAAGATGGATTGTTCCTATAAAGCACATAGTATGTTTACTGGTATCGT AAGAGCTGGAAGAGAGCTCAAGTTTTGGTTTACTTTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA GTC
M18079	52 GA ---	---	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGATTGGTCCCTTTTATAAACATTGGTATATTCCATTATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 TC ---	---	TAGGGATCTGTGCCAGGCCATTGGACACAGCCACACCCACTCCACCCCTGTAGTCTCCACCC TGGACTGGTGGCCCCACCCCTGCGGGAGGCCCTCCCATGTGCTG[T/C]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTGCTTCTAATA GC
M21539	114 TG ---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGATCTGCCATGATGATCCCGACAGCAAAAT[G/G]GTTTCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 AG ---	---	CCTAGCATATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTATTTCCCTGACTTC CTGATTTTCTTTCTCAAGTGTTACCTACTAAG[G/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 AG ---	---	CCTAGCATATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTATTTCCCTGACTTC CTGATTTTCTTTCTCA/[G/G]GTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 CG ---	---	CCTAGCATATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCTCCAAATGTTTCTCCTCTCACCC TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTATTTCCCTGAC TTCCTGATTTTCTTTCTCAAGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 GC ---	---	TAAGGACGTGTACGGAGGCCAGTCACAGTCACAGCAATCCACAACCCACTTGAC[G/C]AATGCT TGCCAAAGCTGTTTAAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTCTTAGAAGAAACCCCA CAATAAAGCAATTCAATC
M81695	34 GA ---	---	ACTTACTACCCCTACCTGTGAGGCTGACGGGGAG[G/A]GAACCACTGCACCCAGAGAGGCTGGG ATGGGCTGCTCTGCTTTGGGAGAAACGCTTGTCTGGGAAGGGCCCTTGTCTTGTCAAGGTTT CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166 C T ---	---	CTCTCCTTTATTTAGCATGGAGGTTTAAATGGAGGATCTCTCTTTCTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAATTT TATTTCCAGGCTATTTAATACGTACTTTAGTC/TJTGGAATTTCTATGTCAATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39 T C ---	---	GAGGCCATTATGAGGGTCTCTACTTCAGGAACACCCCA/TJGACATTGCATTTGGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGTTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTGGCCCAAGAAAGCAAGGAACCAATTTAAGACTCTGCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGCAAGAGCGCAAGATGATTTTGAAGGTTGTATTCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCT/CJACATCTGCCGCCCTTCCAGCCCTTCCCAAGCCCTCTCTTGTCTTCTTC ATTCAATCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATTTCTT/CJGCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGGGTTCTCTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTTCAAATGTTCTTTTAAATGGTCAGTTTAAAGAACTTCAACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCCAAGAGATTT/CJTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAAAGAAATTAATAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATGT/CJTGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122 T C ---	---	TCCAATTTATGGTCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCTTGGAGACTGAGCGATGACACCACACT/CJTGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAATAGACTCAGCTATGTCCTGATTCAGCTGGGTAGTTCTAGAACTTT/CJAGAAG CTCCATCTTTTAAATGTTTTATTGTTATGTCCTCCCTCCCGGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGAATAGCAATTAGGCACCTTCC AAGCTTTAGTAGAGAGAGCC

U25975b	164	C A	---	---	---	TCAC TGTGTGGCCTCATACTCTTTTTCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAG[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G	---	---	---	TCAC TGTGTGGCCTCATACTCTTTTTCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G	---	---	---	CAGGGAGAGGTTATTACAAACCTCACAAACTAGTATCATTTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCTATTTTCTATCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTAACTCAATATCCCAACATTTCTGCAATGGCAGCATTTCCGACCAACAAAA TCC
U28413	29	C T	---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTTGCTACAGTACAAGTAAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A G	---	---	---	TAGGGTAGCATTTAAGATTACAGGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A G	---	---	---	TAGGGTAGCATTTAAGATTACAGGAGTCATTAG[C/A]GTGATGATTTTGGACCTGCCGTATAATCT GTTCTTTATCCACGTTAGCCAATTTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A G	---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGACGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTATCAA[A/G]CCCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGAGGAGGAGGATGCCAGCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A	---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGACGTGAAGACCAATGAGACGGCTGCAACCAACA GCC[G/A]TCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGAGGAGGAGGATGCCAGCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 GA ---	---	AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTGTTACAAATGCTAGGTCCACACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCCTCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---	---	AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCAGCCACAAATCTGGTGCCTCTCTCTGTTACAAATGCTAGGTCCACACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCCTCATTTCACTTGACCCCTGCCACCTCTCC ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---	---	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCGAGCTCAGGTGCTGGAGCTGCACATGACTGCATCTGCTGCCAGG GCTGCAAGCAAGTCTTGCTTCTATCTGGGGACGCTGCTCGAGAGGCGGAGAGGCGCGAGAAC ATGCCAGGTGTCC
U37690	54 AG ---	---	GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCC[T/A]G[CCCCGAAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCTGGCCGCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGTCTTT
V00540	39 TC ---	---	TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTCAAAGACTCATTTCTCTATAACCCGCGATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---	---	TCAAGAAAGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACCTGAGCCTCTCTGAGACCCTGTTTAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCTAGAAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAAACCCTGAGATCATCAG
X52011b	148 CT ---	---	AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAATTCGG AAATCTGTTGTGCA[C/T]GCTCAATGAAACGCCCTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 AC ---	---	AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAA[A/C]GTTGCGAAATTT GCGAAATCTGTTGTGCACGCTCAATGAAACGCCCTTCGGCTTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT



X54741	24 A G ---				CAGGCCACCTGCTTCTCTCCAC A G TGCACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GGACAAATGGAATCCCGAGGCTCCAGGACTGGGCTTGCCAGGCTTGCAATAGCAAGGCCAG GGCAGCTGGAGACGATCTTGCTGGCAGGGCTGGCTTGCCAGCCACCTGGCCCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---				AAGCATTTGCGTTTACAGTGCAATCAGATACATTTTATTTCTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTTATTTGCTCT A G ATACAAAAATCTAAATCAATTTATTGAAATAG GATGCACACAATTTACTAAAGTACAGACATCTAGCATTTTGTCGGGCTCATTTTGCTCAACATGGTA
X86924	147 G A ---				GCGGTGCTGACACCTCCAGAACGAGGTGCTGGGCGCGTCTGCTGGACCCCGGGAACCTCTC CTGCCGGAAGCGGACGGAGGATGGCCCCAACTTGGCTGCCACTTGACTTACCAAAATCCCT TCCTGGAGACT G A AACCTGGTGTCTCAGGAGCGAAGGACTGTGAAC TTG GGCTGAAGAGCCAGA
X78932	62 T G ---				GAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACTTGATTGTATATAGATAAT T G T CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAGCATTTATCTTATCTGAGAAAAATTTGATAAGAAATGGAAGTCAATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---				CTCAACCCATAACCTCAACACATCT C TATCTCCACCCACATCCACACCATCCACCTCCATCC CCAAACCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80197b	99 G C ---				ACCCCACTCAAGTCCAGGCCCGCAGGCATCTTCTGOCCTGCCTTGCTGGCCCCATCCAGTCCAGG CGCTGGAGCAAGTGCTCAGCTACTTCTCT G C ACTTTGAAAGACCCCTCCGACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG
X80197a	28 A G ---				ACCCCACTCAAGTCCAGGCCCGCAGGC A G TCTTCTGOCCTGCCTTGCTGGCCCCATCCAGTCC AGGGCTGGAGCAAGTGCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCGACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG
X85106	150 G A ---				GGCACCCAGAGTGACACAAGTCCAGAGGGAGCGCGCCGCTCGCCGTGTCGGTTCCTTTT CAGCCCCGGAGAGTCTGACCTGGGGCTTCTCAAGCTCACTGGGCCACGCTCCCGCGGCTCT CTTTCTCCCAAGC G A AAACCAATGCGCCCCCTTCACTCGCGTGGCCGTGGAGGCGGGGGCTT CTTTCAGAGC
X87160	128 T G ---				ACCACAGCCATGGTCTAAGGACATGATCGGGTGCCCGACAGCGTGTGCACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCT G GGGG ATCGCAGGAGGAGGCCATCGGGTACTACGCAGCAACACTCAACACTGTCCAGGCTGAGATAAATCCC GGGA

X87344	34 C T ---	---	CATCCCAAGGCACCTGGTGTGACTCTGCTTCTGTC/TACTACCCAGAGCCTCTGCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCCCAAGGGACTCTCTGTTTCCATTCTCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAATCATTTACCGACTTTAGTGCTTTTTT
X87838	179 G T ---	---	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTACCAAGCTGAGTTTCCTATGGGAACAATTGA AGTAAACTTTTTTGTCTGCTCTTTTGGTCGAGGAGTAACAATACAAATGGAATTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAATTA[G/T]CAACCCCTAGCCTTGCTT GTTAAATTT
Z14138	81 A G ---	---	GTTCTGCTGCCTTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[A/G]TGAATGTGCCTCCAGCGGCCCTGTGTTTGACATGTGAAGCTATTTGAT ATGCACAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191 A C ---	---	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAACAGGCTTGGAATCTGGGTAATTAACAAACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTTC CAGTACTGGTTTCCAA
Z23091	159 G A ---	---	AGAACCTGACACAGATGTGGCTGGAGGGGAATCCAGACCCGCTGCTGCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCACTGCCAGCCCTCTCTTCCCTCCTCCTCCCTCCCTCCCTCCG CTCTGTGCTCTTCATCTCAQ[G/A]GGCCCCGCAACCCCTCCTCTCTCTGTCGCCGCCGCTCTCTGGA CTGAGCTTGACGTTTG
11595b	125 A G ---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAACCTGACCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACCTACCTTGCTTTGTGTTGAAGGAGTGGTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCCGTCAACAGACTAGATTGTCTCAATGTCCTTGGCTTGGAC
11595	125 A G ---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAACCTGACCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACCTACCTTGCTTTGTGTTGAAGGAGTGGTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGGAC
1241	131 G T ---	---	TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTTGAA TGCTTGTCTCTTTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACTT[GT ]GCAGGAGTGTTTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAG

1282	130	CT	---			GTGCGATCACCCTACAGTCTAATTTTCAGATGTTTTCATTAACCCCTAAAGAAATCTTGTACCCATTAGCAAATTTATCTCTCCTCCTCACCAGGCTACTCTTTATCGCTATAGATTTGCCQ[C]/TACTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATGGCTCTCTTCACTGAGAATAATGTTTCAAGGT
6810	68	CT	---			AGTATCACACATACTTAATATATAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTTA/C/JAGAAAGCATTTTAAATTTTACAACACAAGCTCAACGAACTTACAAATAGTCTAGTAGTCTGTTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCTTTAAATGTCTATGAACAAGTACAAATTTCTTTTGTAGTTCTGCAGAGCAATGACCCTAAGAAATATTTTAAAGGC
6817	118	AC	---			CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGGTAAC[A/C]JGTGGATACCCCTGTGTCTCTACTGGCCTCCAAAGGCATTCAGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAAGGTGCGCCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212	C	---			CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGAGGAGCCTAGTAAAGCCCCGTCAGTAGTACACATTTCTCTATGTGCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTTAGCAAAACAGCAATAACTTTTGTTCCTATATGACACCTAATATCCA
6819a	166	GT	---			CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGAGGAGCCTAGTAAAGCCCCGTCAGTAGTACACATTTCTCTATGTGCTTCAACAGTTT[G/J]CATATACAAAATTTTCTGCTATTTTGTCTTTAGCAAAACAGCAATAACTTTTGTTCCTATATGACACCTAATATCCA
681xx	39	AG	---			CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTGGGACACAGATTATATATGTCAGACACCCAGCAATGTCCCTTAAGATATGCAGCAAGCACAAATCTGTCTATGTTTAAACAAAAGAAATGAACGCTAGG
6972b	149	GT	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCTTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATTGATTATGGCACAAATTCAGA[G/J]CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGAGAGTGTATGTGTCAGGAAT
6972a	122	AG	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCTTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA[G/J]CTATTGATTATGGCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGAGAGTGTATGTGTCAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598l	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACAGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---			AAAGGTAAATCAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA/GJAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTAATTCCTTGAGGATGCCTT TTAATAATTGATCCCATTAATGTGAGAGATTTTCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---			AAAGGTAAATCAAGTTCCTCTATAAATTATGATTTACAAAAGACAC/GJCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTAATTCCTTGAGGATGCCTT TTAATAATTGATCCCATTAATGTGAGAGATTTTCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---			AAAGGTAAATCAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTAATTCCTTGAGGATGCCTT TTAATAATTGATCCCATTAATGTGAGAGATTTTCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAA/TTCCTTGAGGTTCCCT
7998b	94 A C ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAA/TTCCTTGAGGTTCCCT
7998a	75 A T ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAA/TTCCTTGAGGTTCCCT
8071	119 A G ---			AAATACAGAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAATGGGTTCCCAATAAATGGAATTTTAGGGCAACAAAGTCTAAAAGGCC/GJCAAAAAGAGA AATAGCACCACGTGCTTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGTAATCCACACAGAGCATGCACACATTTTATCAT
8467b	93 C T ---			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/C/TGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTAATG
8467a	70 A G ---			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/GJCGCAAAATCCACTTTGCTGTAAACGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTAATG
8498	84 C T ---			AGGCTTTCAGGTTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/C/TJAATACCTTCAATTAATCGAAAAGAAAAAATTCCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAAGTCTTTAAATTAAGGAGGAGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCTCAATACAGAACCAAGGAATGTAATTTCTTAACCTCAG

WI-18562	29 GA ---	---	---	CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATTT TAGCATTAATCAGAAACGA
WI-18618	51 AC ---	---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCGGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTTGTAACACAGTGCTCGCACAGTTC AC
WI-18683	22 CT ---	---	---	TAAGCTGTTCCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGCGTCCACCCAAA CAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75 GA ---	---	---	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTCTTCCGTGAGAC
WI-18553	94 AG ---	---	---	AAATAAAGTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]ACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 TA ---	---	---	GTCTATTTCAAATTAGCTAGACCCATTTCATTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTTAAATCAGTGCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94 GA ---	---	---	AACITTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACAAAG[A/G]ATATAGCTTATTGGTGAATCTTCATCCT
WI-18723g	71 TC ---	---	---	AACITTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAAG TGGT[C/A]ACAGGTACATAGGTAAACAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ---	---	---	AACITTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44 GA ---	---	---	TTTATTACAATATTAGGTGGCACATAACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76 GA ---	---	---	TTATTACAAAAAGTGATATTGCAGAGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGAGCCTCCAGGTGGAAGGGTATTTTATAAAAAATAA TGGAGCTACAACACCCCGC
WI-18535	107 GA ---	---	---	GTAAATAAAGTTTATTGGCACAGCCACGCTCGTTTCATTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGGTG
D17525	107 CT ---	---	---	AGAGTGGTGCAGAACACAGCGCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTTCAGTTCTTCATAAGATGGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAGGTGATGTGTCTACCGAGCAGCAAG

DWU-133c	313 A G ---	---	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGTCTCATGACITTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ---	---	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGTCTCATGACITTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ---	---	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGTCTCATGACITTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC TCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCCTTCAGTGCATCTGGGAAGATTTCTACCCCTGACCAACAGTTCCTTCAGCTTCCATTTCCGCC CCTCATTTATCCCTCAACCCCGACGCCACAGGTTTATACAGCTCAGCTTTTGCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTCATGTGGAATATAAAGAT
DWU-387	169 G T ---	---	GTGTATAAAATGCAACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCAAATCTTTCTGAA GATGAAGAGTTTGTGTTTAAACTGCACTGCCAACAAGTTCACATCATATATAAAGCATTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAATGCTTAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAAAGTAATAACACAATGAAGTGTCATTATTCAA
DWU-447b	172 ---	---	ATTTAGTGTCTTGGCTTAAAAATCAATGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCAATTTAAATCACTGTAAATTAATGTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAAATGTTCTTTCTGTTAG GCCCTTCTTCTTACAAATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-447	85 A G ---	---	ATTTAGTGTCTTGGCTTAAAAATCAATGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCAATTTAAAGTCACTGTAAATTAATGTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAAATGTTCTTTCTG TTAGGCCCTTCTTCTTACAAATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-478	63 C G ---	---	GTAAATTCAGTTTTTTCCAGTTCCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGGTGAGTGGTAT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCTCATACAGAAAATTCTATCACCATACAAAAATTAA A/TJG CAGTATTTATGTTTAAAGCACAGGTGTACCGAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACTTTGAGCTTTAAACITTTAA
DWU-512	131 A G ---	---	---	AAAATCCAGGCATTTGAAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAAGGTGAACCTGCTTTGAATATCCAGATGTGTTTGGTC/AGJ TGCATATGCCAGTGAGCAGGTATGTTTGCCTTTGCTTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTTTATCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTTTCTATACCTGTTGTA ATATACAGTTTTTGTAAACCATATGATTGA/CJ/AGAAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTTCTGCTTTTACAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAACTCTCTAAAAATCTAGTCTCTGATTTGC
DWU-59	94 C T ---	---	---	CATTTCTTTGTGAAGGTAATGGACTCACAAGGGGGAAGAACATGCTGAGATGGAAAGTCTACCGG CCCTTTCTTTGTGAACGTACATTGGC/CJ/AGAGCCGTGTTTCCAGTCCAGGTGCCAGACTCGTTTTG GTAGTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCCGTGATTTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGTTAAGC
EST11	68 C -- ---	---	---	CTTGATCATGGGTGGAATTTTGTGATCTGGGCTTCATGGGATGCATAAAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCCTTCGCTGCATTGCAAGAGGAGAGCAGGTCCTCCTCTGGAGAA/CJ/G CTGCTTCCCAGCCCCACACCGGCTTGCACACACAGGCTGTGAGGCAGGAGGTGGTGAAGACGT AGCTGTAGACCCCAAGCAACCAAGCCCTGGGACCTCGGGGAGAGGAGCCTTTAGAACATGGAA AAGTGGTGCATCCCATATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA/J/GJGAATGAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTTCATAA/TJ/CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT/CJ/AACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCTTAACTGTCAAACCTTTCATTTACTGAGATTATTTTCAGGCCAAT GTGTC/JTJTGTTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTCTCTGTTTCA



WI-18063	105 GA ---	---	---	AGGCTTTAAACTGATAACAATTTGCCCTTTAATCACAATACAAAACTCTGCACCTTTTCATCTCCTTCG CCATGTTTCTGATTTTGATGTAACCTTAAATTTGTTG[A]TCCCTTTAACAATATACTGTAGCTGCA
WI-18078	86 AT ---	---	---	AGTTGAAAGATCAGAGAGGTTATGTTGGTAGTAGTGAACCTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAGATGTGCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90 TC ---	---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTTTCATCTCTTTGTTAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACITTC[GGGCCCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38 TC ---	---	---	GCAATCTGTAACAGTTTTGGTAGTGGTATTACAGAGGATTCITTGTAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAACTACTGACAACAGTTTAATTTGGTCTT
WI-18142	66 TG ---	---	---	TTCAAGATAATTACAAATTGGAAGGGGACCAATAATTCACITTTTAAATCGAAAAATAATCTATATAC[ T/G]CCCAATAAAGCTACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68 TC ---	---	---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACAGATTCACTCCATGCCTGGAGGTTAGTCTGGGG GT/C]CGGCGGGATGGACACAGACAGACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35 GT ---	---	---	TCAATCTGAAACTTGTCTAAGCCAGCATGGGGT[G/TTGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115 GA ---	---	---	ACAGATGTCAGTTGTTGAATGGCCATTAAAGTATGGGGCTTTCTGTTAAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGCTATACAACGGAGGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26 GA ---	---	---	GATTGGAAGGGATTGCTTTTAACTG[A]TGAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18268	88 CT ---	---	---	TAGGAGGAAAGGAGGTGGCTGCCCTGGCCCTCAAGACATGAGAACGGGTGGTGGCTTCCAAAGC TTCTTACTTCCCCATAGATTC]CCTGACAATGTCTGCAGAAGCCTCCAACTGGAAC
WI-18299f	107 CA ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTTGCCAAATTTTTT ATCTATTTGGGCTGAGAATTCACAAATTTGA[G]GAATTCCTTTGGCCAATTTTGACATATCTG CAG
WI-18299e	101 AG ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTTGCCAAATTTTTT ATCTATTTGGGCTGAGAATTCACAAATTTGAAGAAATCTTTGGCCAATTTTGACATATCTG CAG
WI-18299d	77 GA ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTTGCCAAATTTTTT T/G]ATCTATTTGGGCTGAGAATTCACAAATTTGAAGAAATCTTTGGCCAATTTTGACATATCTG CAG
WI-18299c	67 TG ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTTGCCAAATTTTTT T/G]ATCTATTTGGGCTGAGAATTCACAAATTTGAAGAAATCTTTGGCCAATTTTGACATATCTG CAG

WI-18299b	52	GA ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTTGCCAAATTTT TTTATCTATTGGGCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAATTAATTGACATATTCTG CAG
WI-18299a	48	CT ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/T]TTGGTTTGCCAAATTTT TTTATCTATTGGGCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAATTAATTGACATATTCTG CAG
WI-18307	76	GA ---	---	---	TCAACTTGTTACCAAGTTTAGCAGCAAGAGGATACCTCTCTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCGCTG[G/A]TGCTATGTAAAGCATCCAGATGGTTTATTGTACTCTGCAATCTGCTTGGICAC
WI-18324	72	CT ---	---	---	TTTGGTATGAAATCTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAGTG
WI-18350	48	TC ---	---	---	ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAATGTTTTCAGAT[C/T]TAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACAAGTCA
WI-18395	77	GC ---	---	---	CTTGACATGATCTGTGAAATAACGTGATTGGTTGAAATTTCTGGAAAAATTTGAAGAAATAAATTG ATTATTCAAAG[C/C]TGTCATTGGTTTATACATACTCTCTCTCTTAATGCAAGCTATG
WI-18398	62	GT ---	---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAGAAAGAAACAACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATTAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18398	21	CA ---	---	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCTCTTTTCGCTCTTTTAAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGACAAAGTC AATGAAAA
WI-18409a	20	CA ---	---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAGCTCTGGGGCCCAAGAGGCCCAAGTGCTA
WI-18442	62	CT ---	---	---	AAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAAAAAAGG TTTATAGTGGGAGAGAGGA
WI-18452	38	GA ---	---	---	TTGATGTTAATACTGTCTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTTCCAAACCA
WI-18489	102	AC ---	---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAGATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93	A ---	---	---	CTGGTGGGAGGAAACAAATTTGTGGTATATTATACAAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGTATGGGAAAGAAACCAATTCA TAAGAATACACAGTACAT

EST5	93 A ---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTCATAATGGAACCTCTTCAGAAATAGAAAGGAA CAAACTGAAATCACAAACATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTCTTTTGAACAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A ---	---	GGACAGGACCTCTATTCGCGCTGTGCAGCAGCGGCTGATGGACTGAGGCCCGCAGGGATCTGGGCC CTCTCTCAGGGCGTCTCAGGACCCAGAGCTGTTCTGCTTTGAGTTCCCTAGAGCTGTGGGCCA GATAGCTGTTCTGAGTTGCAAGCACGATGGAGATTGGACACTGTGTCTTTGGTGGGGT
WI- 18740c	104 GT ---	---	TCCTCATTGTTGGGATGATGAGAAGAAATGATTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCACATCATGTATCCAGTAGTG[GT/TAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---	---	TCCTCATTGTTGGGATGATGAGAAGAAATGATTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCACATCATGTATC[GT/AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 CT ---	---	CCAAAGTCTCTGCTCATAAAGAGTTTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTGCCCTTCAATTTACAGAGGTAGCACA[GT/TTGATTCACACAAAACCCCTTCCCC TTTTAAATGATTCTGTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCTCTT TGAAGCAATGACAAGCACITTTACTTTACGGTGGTTTTGTTTTCTTAT
WI-18746	114 GA ---	---	GCCAGCAGCTGAAGTCTTTTTCTCTCTCGGCTGGAGAACATCAAGATACCTTTGGTGGATCA AGCTTGTAAGTCTGACCGTTTTTATATTACTTTTGTAAATATCTT[GT/ATCCACATTTCTCAGCT TTGGATGTGGTTACCG
WI-19112	212 GA ---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTATCTCATGACAAACACACAAAGAACCCGAGACAAA TCTTTTGGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTTAAAGAACACACGGTGATATCTTTGAG GGTGACAAGGG[GT/ATCTCTTCAACAGTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC ---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTTCTTTCTAGCCCTACTTGAATCTTGCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTATTAAACTGAAATTTTC TTTTAAGCTAACAAAGATCATAATTTT[GT/ATGATTAGCCGTGTAAC
WI-19057	175 GA ---	---	CCCATTATTATAGCCAGTGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTCAACTCTTCA GTCTTCTGACGGCGGACTTACCGTGACAGCGGAAGTGTATTGTAGTCCAGGACCGCAGCCACTG TCTTCATGCAGGAACCAAGTGCAGATCCCCACAGCTC[GT/ATCTCTTCTATCTTGGTTTTGGCCACA

WI-20103	168	CT ---	---	TGGGACTCCAACTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGCTTCTGGGCTGGAGGCTGGTCTCTCCCA[C/T]TTCATTCGTCAAAGCTTCTTGAAGGAGC TGGTTGACTCAACTTGTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	GA ---	---	GGCTTACCAATTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACCTACCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116	AG ---	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAAACACGT TTTAGTCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	AG ---	---	GTCTCAAGGGGGAGAAAACACTGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGAA[G/A]AAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	AC ---	---	GTCTCAAGGGGGAGAAAACACTGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	AG ---	---	CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA[G/T]ATAACATTAGAAAA GCAAAATCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	TC ---	---	GGCAGTTGGAATATGGCTATACGAACCAAGAGTGTATACAAAATGGAGTGGTCATCAGGCAATA ATTGTTTCCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGACTTACACATTCAGTTTGACAG T[C/T]GAAAAACCAACTGGAGCTGCTTTCCAAAGAAATGTTCTGTGCTTCAAAATAGGAATTCATG TTATTCTTTCTTGCCTTAAGCTCTTATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	GA ---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAGCTGGGAGCGT GGGCTCAGCAGGCGTGTACCTCCATCCCGTAAGACCTCTCTCCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	GA ---	---	AGCAGTGGCCTTATTCATCCCAACACAGCTCTTGACAGGCTGCCTCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTGTCTTTAAGTGAAAAATGGTCGAGAAAGAGGCACC[G/A]GGAGCCG TCCTGGGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTGAGATCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCTTTTGGCCTTTTGCAACC

WI-20148	31 T C ---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/CJCATTTGAGATAAAGTCAATGCCAAACACTAG CTCTGTATTAAATCCCATCATTACTGGTAAAGCCCTCATTTGAATGTGTGAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATTGGTTTCACGCCCTGAGGCAATTAGACACTTTGGAGATGGCATAACCTGTCTCACCTGGAC TTAAGC/GA/TCTGGCTCTAATTCACAGTCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAG GAGCCACCAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/G/TATTTAGAAATG TACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/G/TGACGATGATGTGAATTTAGAAATG TACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18771b	75 G A ---	---	---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA/G/A/AAATAAATGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/G/JAGATGTT GGAAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTGGTCTGGTGTTGTATGAAATTTCTGAG GC/C/T/GATTAAATCTTTTCATTGTATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCCTGTAGCCCCCTCACTTTCTGTTTTCACATTTGCCAATGTA/C/ATCGGGTTTGGTTT TCTTGATTATTTAAACGGTTGTGTTTCTTTTTCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGAOCCCTCCCTTCTCTGCTTCTCTCTCATCA TCATTTCCCAACAACATCCTCTGCCA/C/ACACACAACAAAGTAAGTTTCATTTGGGCAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCTGCTGCCAGTTCTCTCACTGCGGGGACC AGCAAAAGGCTTCTCACTGGGTTGGTCAAAAG/G/ATGTCACCTTGGCCTGTGTCATCCACAGAGGA TGTTGTTCAAAACCAGAAATCTTTAAACGACTGACC/TTCCTTAAAAACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCTGCTGCCAGTTCTCTCACTGCGGGGACC ACCAGAAAGGCTTCTCACTGGGTTGGTCAAAAGGTAAGTACCTTGGCCTGTGTCATCCACAGAGGAT GTTGTTCAAAACCAGAAATCTTTAAACGACTGACC/TTCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTAGGTCCTGGAGAAATGTTGTAGGGGTTATTTTTTAAATAGTTCATAAAGAAAT/ GACATAGTATTCTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTAGGTCCTG/CJAGAAATGTTGTAGGGGTTATTTTTTAAATAGTTCATAAAGAA ATACATAGTATTCTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTAGGTCCTG/CJGGAGAAATGTTGTAGGGGTTATTTTTTAAATAGTTCATAAAGAA ATACATAGTATTCTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC/CJCTGGCTG TGCACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTAGGTCCTGGAGAAATGTTGTAGGGGTTATTTTTTAAATAGTTCATAAAGAA ATACATAGTATTCTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19106	247 T C ---	---	TTATCCAGCCCTACCCCTTGTTAGTATTTAGGAGACAGTCAAGCACTAAAGTGCGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCCTTTGAGAAAGAAATAATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAAT/CJTG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/CJGTGTTTAAATTAATTCACAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCCCTTAATAAATTTAAGTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAAATTATTATGCCCTCTTCTCACAGTCAAAAGGAAGTGGGTTGGT TTTTGTTGCTTTTATAGATTTATTGCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTA AAATAATAAATTTGGGAAAGGTGTA/CJACAGTAGCCCCCATCAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCCTCAGGAACTGGAATAAGCCTTCGAAAGAAATTGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTGTTGCTGATTTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTGTTTAAACCTGTACATACTTTGAGTTCA/CJCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGTAAGAACGTGCTTGTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---			TTTGTGAGTGTGCCTCTCGCAATGCCATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAATTTGTCTTCAAGGACATTTGGTGAGAGTCCCAACAG ACACAATTTATACTCGACAGAACTTCAGCATTTGAATTTATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGATTAACATATCTTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTTGCTTATTTATAAATTCATTAAAACACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCAGTTGATTTTTCAGTTATTTCTGAGTGTGCAGACAGTATTTCCGCACTGTATTAAAT GTAACCTTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTTTA/CJATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGAAT
WI-18851	90 T A ---			GCTTCAATTGGCGATTGATTCAGTGCACCAATGTAAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGTATCTT[A/GTAATATAGGATCCTGGAAATGAGACCTGGTGAA
WI-18821b	76 T C ---			TCACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/GGGGGTAGCCATTGTGCAGTCAATGCCCGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 CT ---			TCACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A/CJTAGAGGCTGGGGTAGCCATTGTGCAGTCAATGCCCGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTCTGCTGTCCAT[C/G]ACTGTCTTTTGAACACAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTCTCCATCAGCTTG CTACCTTACCCACACTTCCCTGTATTTGCGTGAGGACGTGGCATCTTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---			TGGAAATTCCTTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAAGTA TGG[C/C]TAGGGAAACATTCCATCCTTGAGTCAAAAAATCTCAATTTCCCTATCTTTGCCACCC TCATGCTGTGTAAT
WI-19037b	155 A G ---			CACGGTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGCCCTGTATGACGGCAATA TCCCAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGAAGTGTGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---			CACGGTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGC[C/A]CCTGTATGACCGCGCAA ATATCCCAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGAAGTGTGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---			TTGAGGAGGTGGGGTGAACCTGCTCCTTGGCAGGGATTTGTGACACTGCATTGCTGGGCTGTTCCTC C/GGGGCTCTCTGGACCTTGACCCGTGGATACCAGGCCATGTGCCATGTTATTTGGGCTCTGGAGGG TGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCCTGTGGCTTATGTCACCCACAGAGGGTCTCTGAGAGTCTGGCTGCCTGGGATGCCCTGCC CCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGAAGCAGAG/GTCTTCTGCTGGCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTCTCTGTGGCCACCAGGCACTACGGCTTCTCTCC AGATGTGCTTGGCTTGCCTGAGCAGACAGTCAAGTGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTITGCAAAACCAACATGTGCTCTTTTCAGTCAATCACTGTTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAAATTTTGTAAATGTGTAATAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCA/C/AJCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTITGCAAAACCAACATGTGCTCTTTTCAGTCAATCACTGTTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAAATTTTGTAAATGTGTAATAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/JTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATACATATACCTGAATATAAGTAACTCCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGCAATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCC/C/AJCTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGCGTAGCTGTGTATCTAGGGATTGCACTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATACATATACCTGAATATAAGTAACTCCAAGC CATGAGTAAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGCAATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGCGTAGCTGTGTATCTAGGGATTGCACTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCAGCTCTGCATCCTTGTCTTGGGGTCTGTGTACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCAGCTCTAGAGGCTCCA/GA/JTCAGAA CTGGACCCCTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGCTTCAGGAGCAGGTAGC AGGCCAAAGTGCACTCAGGCCATCTTCTCCCAATGTCTCCCGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCCTTGGCCTTGCAGCCCATTCAGCAGGGATGGAAGTCACAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGTGACATCTGCCCTTTATCTGTCTCTCT CCCCAGTCTGTACACTTGGCAAGCAGAGTGGTGGCAGACCCAGCCCTTGAAGAGCTTGTAGACC GGAAGGAAGGGCGGTCA/JG/JGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTAAATGAATACTTGTGTG/JC/JCATGTTCAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTCTGGGCATTTGCTGCAATATCTGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAACAAGGACATGCAAGCTCCCTGAGCCAGTTCT



WI-19766b	93 A G ---	---	TGGCTCAATGACTGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC/A/GJGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCTCAATGACTGTGTACATTGGAGAAGCTG/AJTGACGACGATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTGGCTTGGCAITTTGTGGATTGGAAAAACCATTGGAAGAAGGACTTTCTCTGCAA AACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAACCTGAAATTTGCTTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTGGCTTGGCAITTTGTGGATTGGAAAAACCATTGGAAGAAGGACTTTCTCTGCAA CAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACCTGAAATTTGCTTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGAAAGGATCGCACCTTTTCC ATAACCCCTTACATTGGAAGAGCAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGATGTTGGCTCACACGTAAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTGAAATAAAATTTCCATGGTCTTAATTGAACGTGATGTTACTTCTTTTGAATATCCTTTT TTCATTAAATAATTT/CJ/TCTAACCACTCTATGTGTTCAACCTCTGTTTAAACACTAAGATATGGGT TTTGGAAAGGCCACAAGTCACCACTCCATGAAGTGGGCGAATGGTCTTGTGTTTGGAAAGCTCTC CAGGGTGTCTTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAAGCCTGAATATCTCTTTCT/CJTTAAAAATAATTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTGAGACATTGTAATAGTGTCTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGCTGATGAGAAGCTACTGCTCCATTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGCTCTCGGAGGAAAGCGTGTGGTAATATTGGGTGACGTATGC ATCCCCCATGCATTGGTTTJGJATGTCTCCAGTGAGCTGTGGCAAGTCT

WI-20113	60 T C ---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAAAGACCTGAAATACTGTC/GGA AACAGTAAAGCAAATTACCACAAATTAGGAGGAATTTTTCAGACATAGGATATTTAAACAT CACTCAAATACCTGGAGCATGATTCAGCAATAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CAGTTCCACAGGAGAGACACTTGACTTCATTAAAGGCAAAG/GC/TCTTACTCTGTACTTTTCCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	CCTGCAATCACAAAGTGGAACTAGTTGATATTTGAAATCATACTTGATTAAACCACCTTCAGAAA TTCTATTC/JAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGTAAACATGTTTGAAGATTCCTAAGTAAGTATTGACGACTGAGACTAGTCGGGCAA GTCATGAGACCCCTTAGCTGATCTCAT/JAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGGTGAC/JGTCTCTCCAGGCTCATATGGATGTCT CGAGGTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCTCC
WI-19348b	98 G A ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC/JA/GTACGCTCTCTCCAGGCTCATATGGATGTCT CGAGGTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCTCC
WI-19635	98 A T ---	---	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTAT/JATCTTTATTGTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTCGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCCTT T
WI-19641a	46 A G ---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/JGJTATTATAGTCTCATGTTT TTAATTTATGAATAACGTCGTGATTCATTTGATTTTGATTTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGATGAGGTAGTATTTAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTTATCCCTTC/JA/GGGTAAACCCAG GACTATTGCATGAGCATTCCTTAAATACGTATTTGATGGACACAAGTTTTCATGTCTATTA
WI-19673b	180 C T ---	---	TCTGOCATGATCACATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCTATGCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCAGTGTGAAACATTTTC/JCTGTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAAAACACAGCCC

WI-19673a	35 GA ---	---	---	TCGCCATGATCACAATTGTGATGAAGAACATGATG[A]TCACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGAATTTACCTACCCCTGCTTTTGTCATCACCAGCTGTAATCTAAT AGTGAAAGGCAATGATGTCTCAGTATCACTGTGAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAACACAGCCCC
WI-19724	35 AG ---	---	---	TTTATTTGGAAACAAAGGATTGTAATTTGGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196 TC ---	---	---	TCCTCTCCCCCAACTAGATGGTATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTTCTTGATTGCTTCATGAGAAATGGTGGCTGGGATGGAGTGACATTCCTTGCTGT GGTAACTGCAAGAAAGGAACACAGGCAATGATTCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85 AT ---	---	---	CTTTCCCTCATCCCTCTCCACACACCATCCCGGAACAAGTCTCCAGGATTCCTGCCCACTGGC CATTTGGAGTGTGTC[A/T]TTGGGTAGCAATGTGGAACCAACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTGAGGGCCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCTCATCTCGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 CT ---	---	---	CAATGGACTGAATGAGTGGTGGTGGGTGGGCGACACACACCTTCAATACACGTCAGGTCG CTTCCAGTTTAGAAAACAGAAATCTGCATCTCAGCTGAGCGCAGCAGAGAGGTC[T/CT]CTCCTG ACCCAGACGCACTCACGAGCCAGTCTGTTTCAAACTGCAATTAACCTGCGCCAGAGAGTTCAAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 GA ---	---	---	CACAGCATGGTGAATAAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATCAAGTAAGTTTACAGCACACATTTTGGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAACGACCCAGTTCAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACTCTCTCGGGAGGTAGCTGACAAAG
WI-19076	40 GA ---	---	---	TTGGTTGGATACCTTCTGCTGAAAAAAGCAGTTTAA[T/G/A]GTATTCAAAATACCTTTTAAAA GTATCTAGCACAAAGATTTTCTGTAACTAGATTATGTGTAAACCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTCTATCCAACTATCTTGGCTCCTGAAAAACTGCAGA AAGGCACCTGAAAGCTGTTCTTTAAGATATGGGATTCTTTTATCTT
WI-20218	26 TC ---	---	---	CCACACACTCTGGTTTATAAGCTA[T/C]JAGGACAGAGCAGAGATGGAAC TGAAAACAGGCTAG AAAATAACATAAATTGGAGGGGAACAGTGGGATGAGAAAGAATGACAACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTATCTACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 TC ---	---	---	CAACCTTTTGCAGAGGGGAGCTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAAATCCTCTTTTAAATATCTCCAGGCTTGAATGGGAGGGGCTGGCTTACCCCTTCTCTTCCA TCCAGTCTATTGCCAGAT[T/G]CCAGAGAAAGCGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGGCTTCACTTCTGTGAGCTCTCTCATGCTGGGACTTGTCTTTTCGGGG

WI-20381a	192	GA	---	CTGGAGTGTGCTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGGCTTATGCAAGATGACAGAAATATGTAAATCTGATTGTCCAGAGTTACACTCTGCACTCCCAAGCTACAACAGTGCACAGCTGAGAGGTTCCCTATACTTCTACTACTGTGACAATTTAGCGAJATCCTTC
WI-20572	75	AG	---	AAATGGGAAAATTCCTAACTACAGGACAATGGGTCTACAGTAGGCCGGGAGCCAAACCCAAACAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTTCTTCTCTCAGAAATTAGJTCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCA
WI-20588	133	GA	---	AAATTCATCTTCTCAAAATTTTAAATTTGTTTTAATCCAAAGGTGCCTATTGAATTTCTTCAAAAATAAACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTATCATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGATAAATAGTATACAGCAATCTTACATTTTTAAGAAAATGTGAGATCCTTTGTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAACJ
WI-20593	79	AG	---	GAJGGAGCGGAGCTCTTCCGCATTGAGTGCATCTGACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTTGTACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTTGCTGTACTTCAGJAGTTTTAAATCTGGGAATGAGCATGACGAATGCTCCACCAGATGAGGAAGAAAGCTGTATAAGGAACTCAGGATGTTGTAGGAAGGGGAGTGATGCCAGGCTTCACCCAGACTATCCAGAAGCCATTCATGGGGTATTTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	TC	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCATJGJATGTATCTGTCCCTGCTGCTTTTAGTTAGCAAGGTGTATGAATACTTTAAGTTTTGTTGTTCTTTTCCCTCGTGGTATCAGTGAATACTGATCTATCTCTGGTAGGGTCAATTTACAAAATTGCCATGGAACCTGAGC
WI-19066f	239	AG	---	AAAAGCCACGTGGGATAAAATCACTCACCATCGACGCCACCAGTATTTGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC
WI-19066g	184	CT	---	AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAACTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCCTGTAGCTGAATTAATCTCTCCATAATTCJGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTATGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC
WI-19066f	148	TC	---	AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAACTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCCTGTAGCTGAATTAATCTCTCCATAATTCJGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTATGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC
WI-19066f	148	TC	---	AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAACTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCCTGTAGCTGAATTAATCTCTCCATAATTCJGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTATGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC

WI-19066e	147 GC ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAAATCTCTACGAGAACTGG CATATGTTCTGG[C]/CJTGGTCACCCTGTAGTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066c	100 GA ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATC[G]/AJTCTTAGCCAGTCCAAATCTCTACGAGAAC TGGCATATGTTCTTGGTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066b	87 CT ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTTAGCCAGTCCAAATCTCTACGAGAAC TGGCATATGTTCTTGGTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066a	72 CT ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTTAGCCAGTCCAAATCTCTACGAGAAC TGGCATATGTTCTTGGTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-20860	105 GC ---	---	TTTACAGCGAGTTTTCGGTCTCAATAAGTATGAATCAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGTATATTGTTG/CJTATAAAGGAAAGCATTAAATTA CAGACATATTTACAAGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACA AAGCTATCCACCCGCCCAAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCTCCCTCAGTCTCC TCCACCCGCTCTTCTTCCAGCCTGCTGCATGCTGCACCCCTGGT[C]/TTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120 CT ---	---	TTCCCCAGGGTCTGTATTGGAGTAAGCTCAAATGTA/GJTATTTAACTTCTAGTTGCTTGTTC GTCTTCTTCCAATGATGCTTACTACAGAAAGCAATCAGACACAATAGAGAAAGCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 AG ---	---	GAAAGCCAGAGATTAGCCCCGATTCGGCATCTGTCAACCAGGACAGAA/JTGCATGGACAAGGGA TGAGCTTTACAAGATGATGCACCTTTGGAGATCAGAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTGGGAATGCT
WI-18790	49 AT ---	---	AGGAGGCTGTTCCAGGATCCTGCCAGCAGCCTG/AJGTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGCTAGGCTGGACACAGGATTCAGAAAGACACCAGGCTGCACA GAAAGCCAGATGGAOCCTGAGTGTGGTGCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA
WI-18987	35 GA ---	---	

WI-18919	26	CT	---			TTGGATGAAACACACAGGGATTCCGGAC[CT]GCCAGACCCCAATTTTATACCTTCTACAGTG TTGTTTGTTGTTGGTTTTATTTTTATACCTTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64	GA	---			CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[GA] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	GC	---			CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	TG	---			CTTTCTGGTCAAGGCTTTGGACAT[GT]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAATTTACAAGCCTGGATGAGGCTACTGA
WI-19178a	170	GA	---			TCAGAAGCAGACATGGCATCTGTTCTGCTGCTGTTGGTTGTGTAACCTTTACAGAGACCTGAATT TTAGAAATGCCAGTGCTGCCAGAGTGAGTGAGTAAATCTGCTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCAAAACATATCAACCA[GA]TAGCATTAAACCAATTTATTTCTGTCCTT AGTGCTGAAGATGCTCACCAGTTTTCTGTGACAGTAAGGCAGCATGCT
WI-19212	46	TA	---			CCAAGTTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[TA]GTTTCAGAACCCAAATGT CCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATATGCAGATGGCCTATGGAATATGCAGCTGC ATAATTAACACATTATCAAAAGTCCTTTACAAATTTATTTCCGCAGCATGTCAGCTAAGTAGACCCA ATGGGGAGAGAAATGCCTGCTTTCTTCCCTCTTTTCTGCACCTGCCATAT
WI-19183	210	GC	---			CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAGACACACATTGGATG GCAGCATGGGTTTCTCCCATTTTATGGGCATGAATATGTGGTTTGAATTAAGGAACAAGCATTATT CCTTTGCCAACAGCCTCACTCTAAGAGGCTTTTGTGAGTCAAGCAAAACACTTGCCTGCTCTGCC CTTGGAG[GC]TGCAATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	TC	---			TTGAAATCCCAGTCTCTGCCCCCAGGCGGGTCTGTCCACCATAGATATGCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTCCCTGTCCATACCATCGATGTTCTTT TGTTCAGAGCAATGTTTCTGTATTTCTGAAACTGGAACCTGAACCACTTGGCTTTCTCTCTAGTCAAC AAGCATACTT[CT]CTCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	TC	---			GTCTCCCCAGAGTGCTTCTGCACCCCCAGCCCTGTCTGCTGTAGAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGGTGCCCTTAGTTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGGCCCCAAGCTCATCACACCCAGGGGCCATCTTCTCAATACAGCCT[CT]G CCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGCTTGGCTGCTGT
WI-19135	20	GA	---			CAGTTACCTGCTTTGCCCTC[GA]AAAGTGTGCATCAATTTGTAATTTTAGTATTAACCTCTGTAAAAAGT GTCTGTAGGTACGTTTTATATATATAAGGACAGACCACCAAAATCAACCTATCAAGAGCTTCAAAAACT TTGGGAAAGGTGGGTTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTTGCCCATATAAATGCTGTATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	---	TACACAGAGGGTGCACCTGGACTCTGAGGTTGGGTGTGGAAAGGGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTCTGTGACCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CAGCTTACCCTTTTATAGGGGAAGAGTGTACACTCTCTGGCTATCTCAGGGGAATGGGAAAAAG AATCTTTCAAGGGCAAGAACTCTGTGGAGGATGTCTGTGTATGTATACT
WI-19144	222	G C ---	---	---	GTCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTACGCTTGTGACCTCCAGCCTTCTTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTCTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACTAGC[A/T]TTTCACGGGTGGGCAC ATGGGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGATTTACACGAGGGTAGA C/TGGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACTAGC[A/T]TTTCACGGGTGGGCAC ATGGGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACTAAACATGAAGGAAGGGTGCCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG[T/C]GGCTCATGGCAGAGCATT CAGTGCCACCGTTTAGG
WI-19235	173	A G ---	---	---	TTCAGGAGGTGGAGTTGCTGTCAGCTCTCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCCTCTCAGTCCCAAGTATTGCTGTGATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTTTCACAATGGTGGAA[G]GCTTCATGTAATATGATCAGGACCCAC TCCAGTCTCTGAAAGTGTGACAGTGTCCAGCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	---	CGTTTCCCTAACTCACCAGTTTAGTTGGGATGATTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAC[G/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGACACTGACGTGTCCAGAGCAGCATT
WI-19117	134	A G ---	---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTTACAGGAAACAACCTTGCCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTTCCCTAAGACATTTTTCATTTCATGAATATTTCAAGTTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCACTGAAATGAATGCCGAATTTG

WI-19134c	263 C T ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCAGCAAGGGGTGCAGCCAGGGTGCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATCTCTTTTCAGAGCAC TTATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGAAAGGG
WI-19134a	162 T C ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCAGCAAGGGGTGCAGCCAGGGTGCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATCTCTTTTCAGAG CACTTCATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGAA
WI-19224	112 C T ---			GGTTTCACAGTCTTCCAGGGAACTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAAACCAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCAATATCCAGCGCCAGAAAGACTTCG AGGGAACACTCATTCAGGAGGTGAAAATGATGGATGACTCTCCCAAGATGAAAA
WI-19201	179 T C ---			GCAGCTCTAAGGACCACCTGGCCATTAGCTTGTGTTTGTATGGCATCTCTTCCACCTTGTCTCTC CTTGTCTCTCTGTGTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCCGCCCCACACTTTCCTGTCAGGTGCACCGAAAGGACTGTGGGGGATAAAATTCAAAAAA GTGTGATGTCTGCTCAGAGGTCAGACTCCATGTCTGCTTGGCCTCAA
WI-19034	45 T C ---			GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGAAATTC/ACTTCTATTACATTAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGTGTTGAAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGTATATACACTTCAGCATTTAAGTCTGTGCAATTGAC ATTGTCTACTTATAAATAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25 C G ---			TGTTCTGAGTCACGCTGAGGAGAGTCTTCTTCACTCAGGAGTTCATGCTGAGATGATCATGATTCA TGCGACGTATATTTCTTTGGAAACAGATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTGAAAGTCTAGAACTCCTGTAGTTTTGAAGTCAAGGGGAGAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---			AAAGGAGGGAGAATCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGGAA[A/ G]AAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---			AAAGGAGGGAGAATCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGG[G/A] AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---			GGCAGCAGCTTTTAAATTTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAATCTGCTGAGAGCAGAGCTTTC/AAAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121 C T ---			CAGAGGGAAAGTTTATTGAGTCACCCACAGAGGAACAGAGAAACAGACACAGGAGGTTCTGTGT GCATGGAGGAATCAGGGGCGGNACAGCTGAACCTGCGCAGGACAGAGGGGGCGCTGGACAGCA GCGCATGCCACAACATTCA



WI-18017	87 C A ---			ACAAAGAAATGGAATAGGTTGGGAAACCTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATTAATAATTATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTTCAGAAACNTGATCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAGATGA
				TATACGGATCATGTATTTGTGTGACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C ]GCCAAATTCCTCTTGGTTCCTTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18254	64 T C ---			CAATGGGTGGACTGAGTATAAACGCATATTGAGAACAAAGACGGCTTCTGGCCNCTCTGCGTCC AAGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTGGGTGGTTTCTCAG
WI-18265b	117 C A ---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTTCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18295	40 C T ---			GGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTGACACGGTGGGAGACACAAA[T/ C]GAGTAATTAACAACATAATTTTANATGACAGTGCAATTAATTAACGCTCTGGGTAAGCCAGAG GGGAGGAGGGGCTTTCA
WI-18459b	64 T C ---			TTTATTTAAATTTGCATCTCGAGATAATAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGCGAGTATCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-22585	56 A G ---			GGCTGTGGAGTAACAGAACTTGATGGAAATTGGC[A/G]TCTGTGTAGATGATCTAAAGCTTTC AGACAAATGGCAGA
WI-21155	36 A G ---			GCCTTGTCTCTTGCTGCTCAGAGCCTCAGATGGATACGACAGAACTCTCTTTGAACCTTTTAT TTCTCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGAGGTTCTGTGTGCACAGACAG GGAAACAGGC
STS- F02766b	88 G A ---			GGCAGGATCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTATGTGTATTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-19888a	98 C T ---			TGAGACCATCCTCTCAACAAAGATCAGTCAGTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TTGTGCACACAGTACAGTGACAAATCCAGAGGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-21485	82 C T ---			
WI-20601a	125 T C ---			TCAGAAATGCTTCCACTGCCCCAAACCAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAAGTTAAAGAAAGGTACCTCTCTGGAGTTGCATGACAGGATTAGTCTCTCTGTTT[C]CTGGT GCAAGTTTGAACCAAGTATTATGTACCAATTGCATGACAGCATCTGTTCCCTGTGATCCCACTAG

WI- 20561b	94 T C ---	---	---	CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/CJGGAAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---	---	---	CGTTGCTTATTAAAGATGGCTGTTT/A/GJJAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTA TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---	---	---	GCTTTCATTTTCTGTCACCCACCCCTGTCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AT/AJATAAATCTATATCATATATTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---	---	---	GCTTTCATTTTCTGTCACCCACCCCTGTCACCAGTTATGTTGGCCTTCAATATATGGCGTT/AJTAGAA CATATAAATCTATATCATATATTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---	---	---	GCTTTCATTTTCTGTCACCCACCCCTGTCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---	---	---	AAAGATTTGCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGGC G/AJGTGAACATAATGTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	---	CTGGGAGCAAGTAACCATTTTAAAGAAATACTCTCAAC/A/GJAGTTCTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACATAATCTTTGTATTTATTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---	---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTAAGTGGTATGG GAGATTGGATAGAT/CJGCGCTAACCTATCTCAATTTTAAGTAATGAGCAA
WI- 22091c	205 G A ---	---	---	GGCGTGATTTGATGCAATGTCCACCCAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGAGAGCAATGTCATGTACATACAGCATATTACCTCCCGCTTAAGTGACTCATAATTTTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAAAATGTAGGCTTAAGTGGTATTACTTGAGGGCA ACA/GJAATACGGCTTAACACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---	---	---	CAACTGCTGAGGCTTTCACTAGCTGATTTATATACTCTATATT/TAJAAAAAATCTATAGTCTG CAGCTTTTGACATACTTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGGCTTTTGTAGCTTAACGTCTTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
WI-21778b	155 T C ---	---	---	AAAAATCCATAATTATTGAAACCCAGTTACAGAGAAAGTTCGTAACTTTTTATTGAAATTATTGAC TCTGCCGGGTGCTGTTCTGGCTTTCAACTCCAGTCTGTCATGCCCCGTGTGTAGTGGGGTCCCCAG GTCTGGGCTTCTGAGGCTCTTCGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	---	TGAGTCAGTGGTCAGATGGGCGAGTTGCGCTCAGCTGCGAGTCCCTACTCCGGAACACTGTGCGCTCT CAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGCGAGTTGTTTCTAGTACCCATTTAGCCCC ATGGCTCTTCAAGCCAATTCACACTGGGAAAAACACACCCTCACAAGATGCCTATCCATTTGAGTTTC ATACAGGTTTTAGTAGTAGTAACATAAAAAACATTTTAA/CJAATTATCTA
WI-21449b	222 C T ---	---	---	AACAGCAGCAGTCACCTCCAAAATGCAAAAAAATTAACAATTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAAAGANTTGAAGGTACAACAGAAATCAATCAGCAGCACTGGAGGGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAGCTGACAAGAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCAC/CTTGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	---	GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAAACCGACTCCAGCCTGGAAACCTGCCCTC CCATCCCTTGTAGGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGAGTTCTGCCAGGGCAAGG AGCTGTGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---	---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAACCAACCAACCAACCAACCAACCAAG ACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGTGTG/AJAAATTTTCATGAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAACCAACCAACCAACCAACCAACCAAG AGAACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGTGTGAAATTTTCATGAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21809b	146 G A ---	---	---	TCATGAATATGCAGCTCCATAATCTTCTCCCTTGTAAACCGTCAGTCCGTTCAAGCTGTAAA AACAGCCCAACCCCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTCAAAG/GAJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAA[C/T]GTGCAGTCGGTTTCAAGCTGT AAAAAGCCCAACCCAAAGACATCACAGAGGCAAGAGCAGTGCGAGTGAGAGGGAGCCTGTGA AAGGATGTTTCAAAGGAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGGCTAAATCCCTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTGCTCTTGTGATCTGT[G]ACCTCACCCATGCTGCCACCTNAGTTCC CACATTTCCCCACGCTTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCTTTTAAAGGCTCA CAACACTAAAGATTTACATGAAGGTCGTGATTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG TTTC[G]TGCACTGGTACAGAACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCTTTTAAAGGCTCA CAACACTAAAGATTTACATGAAGGTCGTGATTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACTGGTACAGAACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGGNAATACTTATGTGACTTCTTGATTTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGGTT[A]AATACTTATGTGACTTCTTGATTTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAAGGA GCACAGGTAGTCCACAGATA[G/A]GACACAGAACCTCAAGCTGTGAGGTCATTTGTAAATTAA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAGGAAC AGATGTTAACAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCAT[A]ACAT TGGCTGGAATGAGGTGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGACAGACTACATAATGAGCGGTGAAGGGCTGGCTTCCCTCTCCTGACAC CAGCAAGGGGAGGCCACCATCACCGGCCCTGCCCATCATGATCATCCAAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGTCTC[T/G]GTGTTTAAATCCAGGTTAAGCTATACACGTTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAAGTCCCTGTGATGGGAATGAC

WI-21681	117 GC ---	---	---	GCTTAGTCTCCACCCCTTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAG/CJTTTTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 TC ---	---	---	TCAGTTTAAACACATTTCATCAAGGA/T/CJAGATTAAATTAATGTCAGGTGAGCATAAAAGGGAGATTA TAAACCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTATTATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG ---	---	---	TGCTTGATTAAATGTGGTGTACATTATCTATTTCACAGATGGAAACAGAAAAATACCAGCTTTTTT AAA/A/GTAGCAATATCTATTATATAATAAATATTGAAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTTGTGTTGATTTTCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGTGTGTAAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112 GA ---	---	---	TTGCTATAATTTCTTAAATAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGA CAACAGTAAACATACTGGACACCGTTTCAGGCATGAAGGATACA/G/A/CAGTTAATTAACTAAAG GAACAGAGTCCCTGCATTCTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTCGGGGCC AAAACCCACTGAACCTACCCAGCTGAAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97 CT ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAGGGTGAATAGCCCTGATGACGACCTTCGCGTCATACTAT AATGGTTAATAACAGCATTCCTGTCTACCC/C/TJGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTCCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAGGGTGAAT/CJGCTGATGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTCCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---	---	---	TTACCTTCCAAACACAGGCCACTTTGGAGAAAG/GTJAAGAGAATGCTATTATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCGCCACAGAACC TTTGCACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197 AG ---	---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGCGAGGGCTC TGATCCCTCTTCTCAGCAGACAGACCATCTTCAACCCTCCTGGGAAGCAGCATTTGGAGCCTACACCA CTTGCTCTTCTCACCAGGGTAAGAAATGCAGGTTATTTGCAGAGGGGAGTGAGTCTGGGAA/GJG TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCAGCACAGCACCATTCTTACCCTCTCCTGGAAAGCAGCATTGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGTAGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI- 22663c	139 GA ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGGAGGTGAGCCGGCTGCTGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACGTGTGCACCTTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTGTGAATGTGGGT
WI- 22663b	55 CT ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGGAGGTGAGCCGGCTGCTGCTAATCTT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACGTGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTGTGAATGTGGGT
WI- 22663a	38 CT ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGGAGGTGAGCCGGCTGCTGCTAATCTT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACGTGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCCTGCTGCCTGAGTATCTGGGAATCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAATATT/GJTTCTAGTCCATTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI- 22631a	52 TC ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAATCTCGCTTCAGTCTGAT/CJAGCACCATT CAAGTTTAGGCAAGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTTGGACAATCAACTGAAATTTTT
WI-20258	157 GT ---	---	AATCCACACTTTCACGGAGGGGACCAGCCTGCCATGTGTCGCCAGGCTCACAGAGCGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGAGATGGTGACGGCGATTGGAACCGTAAGGCATGACAACG GGAGCCCGGGGTGTTTCAG/GTJCGGTTGACGCAAGGTGATGGCTGGCAGGGCGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCGGGGGAAGTACC
WI-22714	212 CA ---	---	ACTACACATATGCTGATTTTCAACAGTAAAATAACATTTACATTTGTAGAGAAAATCTAGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCCTGCTAAGTCTGACAGGAGTGTGTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/CJATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 GA ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCCT/GA/JCTTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTGGAAGCCATAGTTTGGATGGCAGACTTTTCGGCAGAGGAAAT AGCAAGTGCAAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAACGTTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAA[T/G]GGCTCATACAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGGAAATAAATCCCTAAGGCGAGCAATAATTCTGTCTTTGATCCTTCATTACAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACCTGATTAGAGAGTAGGTATAGAAACCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCCTCGTGTCTGAGCCCTCATCCCCACCCCTCCAAAGCCCTCATGCCACCACACCCGTGCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCATTCOAAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGGAGTGGAGATGGCAGAGATGGGGTGGAGCGAGTGGCTGTGGGTC CTG[A/T]TGGCGTGTGATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTTCTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCAATTGATTTTTTATTGTTCTTCCATTTCTCTGTCAAACTTTTC[A/T]TTTTGTTTATAA ACTGTTTCTAAACTCAGTTAATCTCTATCTGTATTTCCTGTTCCCTGAACTTCTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCAAACCCAGAGCTTCT GATTCAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTCTAAGTGTTCAG ATGCTGCTTGTCGCCGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATTCAGAGAACTGCTAAATTAAGCATAATGATTGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAGCAGAAAATTAGCTTTGAAAATCAATAACATATTTAGTAACACACATT CAITTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCATTTGTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	TTTCCCCACATACCAATGCACCTGTTTGTATAACTATTCGTTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATTAACAATAATTAATAATCTGTACTATTACTGCG TTAGTTATCTAGTGTATTGAGAAAGGAGAGATGATAGTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGACATTGGTGTCTCCTCAGCAAGTCGTAJTCCTCAAAACCTTC CAAAAGAACGAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGACATTGGTGTCTCCTCAGCAAGTCGTAJTCCTCAAAACCTTC CAAAAGAACGAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCAGTGAATACTGTTCAAGTTTCACAGGCTC TCTCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTTCTGGGG TCCAATCACATACTTCAGGTTACAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTTC/TTTCTACTGAATCTTGGGTTGGAG
WI-21122a	42 C T ---	---	TCACITTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA/CTTTAACAGGAACTCTGTTTTC TTATTCAAATGTACAGCCTGACCGTTACTGTACATATTTGCTAGCAGGAGACAACACTGGAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAAATTCCT TTGTAGGTTTCACAGAGCCTATTGTTGGGTTGCT
WI-21254	53 A G ---	---	CAGTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAACCTATTCACAGGAG/AG/CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAACTGCGATGGGTACAAATG/TTTCCAAATTCATACTTAAGAAGGTGGGGAACGGGTCATTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCAATTTCTCTATTC/CTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGTCAAGCAGAGTATGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG/CTTT GAACTACAGTCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCAATTTCTCTATTTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGTCAAGCAGAGTATGGGTGACTATCCTTGCCTAAT



WI-20442	37	TC	---				TCACGTGAAGGAAGAAAAAANGGGGGGGCTTTC/JTAAGGTGGCACAATTTAAGAAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	TC	---				GTGACAAGAGGTGAAGCAAGGACAGGGGCAGCAGGGCCAGTCTCJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	TC	---				ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCCTACATCTGGAATTC/JCATTAC ATCAACGTTAAATTTGTCGACCAGTTCTTATTGCTGATCACTTTTGATTAATGACAGATCCAACAT GAAACTCTGAAGCAAAATGAATATTACCTTGTCTTTCATGCAAAATTAGGACCAAACTCAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTGTACAGGGATCTTCT
WI-21149a	167	GA	---				AGGACCTGCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAGATAGTTGACTAAATACCACCT AAATAGTGGCTTTTTTTTTTAAACAATGACCTTATTTATCTTTTAACTTAACTGAGCTTATATA CAGACCTGCCAACTGGAAGCTTTACAC/GATGCTTCAGAATGCGCAGTATTGCACAATGGTT TGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTACCTG
WI-21376b	188	AG	---				GGTGCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGAAAAACACTTTCAATGTGC TTCCATTTGATGAATTTGTTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCAAATCTGCAGCATTAGGATGAGTTCTC/GJGAAGTGATTCT GAAGTGAACGCACTCATGTCTGCATGGGAACTCTGGGAGAGAGCCT
WI-21382d	125	CG	---				CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGGGGTTGGATCCAGTGGGATNTGGTTCCTCC/JGAGGT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201	GA	---				TCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGGACAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCTTTGGGATGGAAAGTTTCTGAGCTCCCTCCAT CTATTCTGTGGGCAGGAACATGCCAGGGCTGCTGTAAATGGCAGGGTCACTTTACAGGGC/G /ACAGGCATAGTGTGGCCCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156	AC	---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCAAG/CJGCTACATGCATAGACAGTCTCTAAAAGCGTATCTCAAAACATG A
WI-21202a	61	TC	---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTCTGTATAAGCTAAATATGTTGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTCTAAAAGCGTATCTCAAAACATG A

WI-21627b	153	A G ---				GCATGAAAGAACTCCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATAATAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106	A G ---				GCATGAAAGAACTCCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC/GJTATGGATATTTATGCTAGGAATGA CAACAGTAAGGCATTGCAAAATCCAAAGTCATCTAATAATAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75	C T ---				GGATTGAGTCCCACTTGATCTCAAATTCACCTTCTTGATGTAACAAGCTCATCCCTCTAAAGTT TCAGTTT/CJTTCACCAGTAAGGAAAGGTTTGACACAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTGTCCTAGGACTAGGTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTCCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20329a	68	G A ---				CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGTTGAGTGGTACAGAGACAAGACATCAAT C/GAJTCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAAAACAGTAAACCAATCAAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155	T C ---				TTCTGGCATTCAAATGTACATGTAATCCAAATTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAAATCACAATTGTATCTAAGTTTCACTTTAAGAACAATTATAAAGGTAAT AAACTCTAGGTGTACTTAT/CJATGGAAGTGTATTTCCNATTTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAACATTGAGA
WI-21504	147	C T ---				TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGACAATTACAGTGGGGGACGGCCGTTCCGGCTCCAGCTGGGTTTCC AGATGCAACAAT/CJTGGGTTCTGGCTTCTCCACTGGTGGGATGGGGATCGCCCTTCGGAGCTCT CAGGG
WI-21242	115	G A ---				CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACGGCGGAGGGGAGGAGAGAC/GAJCACTAGCTTGGGGGTG GGCAOCCAGCTTCAGACCCCTT
WI-21475c	181	A G ---				TAGCCCTTCTGCCAATCTGGCAATNTGAGGCTGGGGTGGAGGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTACTTGTCTTAAAGCACAG CAGTCTGAAGCTTGGACCTGGCAGTGGCTCTTTGGAGAAGGCA/GJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGTTCTCCACCTATTTCCTCCCTCTGAAG

WI-21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGAGCTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC/A/TCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTTAGAGCAAGACCCCTCCCGTTCTCCACCCCTATTTCCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCTCAAAGGAACCCACCCAGCCCGTGTGAGGCTTGTGCGAGGG CTGTCTTCGGGTTAAAGTGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTCATCACCCTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGCAGT TTC/A/GACATAACATTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCTCAAAGGAACCCACCCAGCCCGTGTGAGGCTTGTGCGAGGG CTGTCTTCGGGTTAAAGTGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTCATCACCCTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGC AGTTTCAACATAACAATTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCTTACCCAGATAGGACTAAGTGGAGGGTGGAGGAACAACAAAGGTGA GGTATC/GGGTCTGTGAGACAAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCAGCAGCGGTGCGAGGAGGAGATGGGGACATTCCTATTCCAGTGCATGTCCTTAAAT AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGACAAAGCGG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTTCCCTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACCTCTTGATTATTTAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA ATTGCTATCAAAATATCAATCTTATTCATTCTTTGTAACATTTATTTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /A/TAATAATTACTTCAGAGTAAATGCGATCTCTTCCCTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACCTCTTGATTATTTAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATATCAATCTTATTCATTCTTTGTAACATTTATTTGTA
WI-21512	54 C G ---	---	TCCTGCTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTC/GTJTAGAGAGGA AAGAGCTGGTCCCTGCTCTGGAGGCAACGTCAGGTCGGGAAAGGCACCTGCTGCTGATCTGTC TCAGTGATGGGAGGTCCTCACTGCCCCACAGGAGCCTCGGGCCAGAGATGAGAAATATGCTGTA TCCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAAACCTCTTAAGGCAGGACAAAGCACTTCCATT ATTCTTAGTTTAGACCAGAACTTTAATTTTATATTTCTCTTTAATACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAGAGGCGAGTGTAA/G/A/JAGTAG TATTCCTACATACCACAGTATACAATGATGCTTCCGTGAGGTTTAGGAAC

WI- 21514b	133 CT ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTCTAGGACTGGTGCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /TJACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 AG ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTCTAGGACTGGTGCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCA/AGTCTTCAAGGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-22020	27 CG ---	---	ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGATATCTACCTGTATGAGGGTACTT
WI- 19576a	113 AG ---	---	TTTCATCGGTTCTTAATACAGTACAATCCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTAACATT[C/AG]TCTAGTTCAAGTATTAGT CACAGAAATTAACATCTGCCAGATGTACACAAATTTGGTAAAAAATACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 AC ---	---	ATACACAGGCCACAATTCAGGATGGAAGGAGTGGGCACTTGAAGTACTACACATGCGCAATA AGCAGCTATCTCTTACCAACCCAGAAAGTTCTGGGGCATGTGATGGTGGCCAGACCCCTTTCCAA GGGAATA/CJTACTACACTAAGCTACACTGTACTGTGAGAGTCAATGGTGAAGGCCACAGGC AGTGGAGGAATGTGATGACTTCACTGTGTTCAGANITTCAGGCCAGCAT
WI- 21574a	235 CT ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTAGGAACCTACTATAGGAAGCAACTTATGAGTG TGTAATATTTGATAGCAGCAACTTTCACCTGATCTGCGAGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGAGGCCATT GGCAGGCCAGGGAATTAAGTGCCTACTTCCCT[C/T]GTCTGTCAGGTGGGA
WI- 21644c	151 TA ---	---	TGACTGCCAAGATTTAGGCCCCAATTAAGGAGCAAGGTCACTTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAATGGATTTTACCACATANTATTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGAT/ATTCATCAAGATCCATGGATGATGCAGTTTAACATGTGTCTCAGC TTGCCTACTGACCACTTTCCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 GA ---	---	TGCTTTTAACTCAAAGTCCAAATAACATATAGACATTTTGTANTAGCTATC[G/AT]TTTAAACA AACCTCATTATGATCACTGTGCAATTCAGTCACCTAAAATACGGAACCATGACTATTAAATAAACA TTTACTGTGTGTGGTTTGTGGGACTGAACATAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 CT ---	---	GACCGAGAAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACT CTTCACTGAGTATTAT[C/T]JAGGACACAATCGACGGATGTAATCTATTGANTTATACCATAGGCCC TATTCATATTTGGCCAAAGGGAAGGTAGGATGGTACTGTGGAACGGGA

WI-21981	61 T A ---				TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAT/AJGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAAACATGCATGGGATAGA
				---	CACCTGTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTTATTACTTTTACATGTGGACAATCTAGTTGAGCGGTTTAAAGGTTAAATTTGG
WI-21660	120 C T ---			---	TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACACGCCCTCTCCACTGCTTACTGTGTACCAAGAAAGGCAGAAAGCAGCTCACCCAAAGCCTAACCTGGCC/C/TJTGCTTTTTTCAGGCTTCAGGATGCCACAGACATACTGGGGAACCTGGGATGCAGGAGAACCCAGGGTCTGTCTTCAGGAGGGTCACAGC
WI-19105c	211 C T ---			---	TGGAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAAGGACACTAAGGCACATGGCTGGTGATCTTTCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGCAGAAATNTGGGGTCCCAGTGGATCTCCCCACAATTC/CJTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---			---	TGGAAGTAGCCCTTCTGGACAGAAAGAATAATTT/CJGTGGTCCATGTGGTTGAGTCTGTTAAGAAAGGACACTAAGGCACATGGCTGGTGATCTTTTCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGCAGAAATNTGGGGTCCCAGTGGATCTCCCCAACACTTCTCTCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---			---	CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGTCTTCCTAGCTTTACAATAAGNGGAGGACTCTGACTGCA/CJACCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---			---	CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGTCTTCCTAGCTTTACAATAAGNGGAGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---			---	TCGGCATAATTGTTCCAGCACCACTATTACTGTTATTATTTCTCTTTGAGGAAAAACCAAGNATTAAGAAATCTGGTTTGAATTTCCATGATGCCTAACTGTTAAATCCTTTTCTTACCAAAAGGA
WI-20934a	72 T G ---			---	ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATAGTTTGCAGAAATTTATCTCTAC/T/CJAGAGACAATTCATAGTTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
				---	CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCAAGAGAA/T/GJCTAAGACAAATGGTCAATATTCAAATGGCCTGGCCTAGTGGTAATTCAGCAGACAAACAGCATGAGAAAGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCAATCAAGCCCTTTACCTCTTAAGATGGCAGATTAGAACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---			---	TTTCCATTTTATTACGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTT/GJCTCTTAACCTCTCCAGGCAAGAAAGGAAAAAGTGATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTTTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAATGGTAGCCCTTCTGGAATAATTTTGTGTAATCTGTTTAAAAAGATTTTGTGATGCATTGCCCCA

[illegible]

WI-22082b	67	C T	---			CAGGACTGGTTGCTGTCCCAACTGCACATAAATGTCCTTTTGTGGTTAGTTGGTTGTG[C /T]GTTTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGGCTCGCTCAGTTCGCGGGAAGGACGTATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTGTGTCACACCTCT
WI-20993	139	A G	---			AACACAACTCCATGCTTTCAAGATTCACACACCCAGATACAGACATATTAAAAATTTACAGCAAT TAAACAGGTAGTTTGGTACAATAACACATATAGCAATGATACAAAATTAGGGGAAAAAACCCCTGG GCTTCTA/GJTAACAAGTGAGTACATTAAGACAGATTTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGGCCTATTTCAAGGCTTCCTAGCTCATCCACACATCACC
WI-21723b	125	A G	---			AAGGATTTTAAATGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTGACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATCCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-21723a	82	G A	---			AAGCGATTTTAAATGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-22132	99	T G	---			CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCTTTTACTATCCTT[G/C]CCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACTCATCTATAGGAATGCTTCTAGTTTAAATGCTGCCCCCAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTTAAATGGGACAGTGGG
WI-21008a	106	A G	---			TGACAGATCACACCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC[G/JAGAGGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C G	---			CTGAGGCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAATAATTTTACATCTCTCTTCTGCGAGTTAAACGTGCCGTGG CT[G/C]CAATACACACCACCAAGCCAGCGTAACCTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G A	---			AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAAATACCAGTGTGCAGCTTTGATTCTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCTGAAATATCTGTAGTGG[G/A]AAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

WI-21079a	50 GA ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G/A]CGCAAAATCAAGT TGTTTTAATACAGTGTGCAGCTTTGATTCCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGTGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 TG ---	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTAAGGAAAAGT[G/TT]ATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAATATAAATAATTTGGTTGCAATTCAGNAAGGGCA TTAACCAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGGTTTAA
WI-21941	79 AG ---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCOCCAAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC[A/G]GATGAGGCTCTTCTGTAAAGTCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTGGGAGCCTCAOCCAGAGAGCTCACTGCATTGACCCACACCCACCACTCAOCC CAGCACAGGCACACGCAGGGCACACGCACACACGNTGCACCTACCAOCCG
WI-18916b	42 CT ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCACTTCTTGGTACCC GGTTAACTGCCAGNGGTGACAGTGATGCCAGGGCTGCCCCACTACTGCACCTGGACACAGCCTCAOCC AATGCCACCTTCATA
WI-18916a	35 GC ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCA[G/C]CTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGTGACAGTGATGCCAGGGCTGCCCCACTACTGCACCTGGACACAGCCTCAOCC AATGCCACCTTCATA
WI-19828c	200 AG ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCTAGCCTAGTGCCAGGCTTCTGGCCCCAAATCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCTCACCACCCCAAAAT[A/G] TCTTTTAATCTTGAAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 CT ---	---	CACAAGAGTCTGTACAACCTTAGGGACACCAGCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCTC ATATCCACCCCATCCCGAGCTCCTGCCOCCGACACCCAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTCTGATCTCTAAGGATCTGAAGCC
WI-19860	51 CG ---	---	TTGACCTAAGCCTAGCATAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCATCCACATAATTTCTGTTGATTTTGCCATTACCCGATAAAATGGTGGGATCTACCTCCCT CCTTGCAAATTTAGCTGGNCTCTGATCTCTAAGGATCTGAAGCC
WI-19899h	80 CT ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGG[C/T]TACAGCAATTTATTCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACCTATTGC



WI-19891c	172 C G ---			TGTTGGTGTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGGCCCTCCCTCCCGG ACTCCTCTGTCTGGAAAGCTGGCTTGNCTCCAGACACAGTGTACATGCCAGCTCTCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTCAGCTCCGGGGCGTGGGGCGTGGCTGTGT CAGCAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---			GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCAAGGGCTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGGCTGCAAACTGCTTTGAGGAAATNCCCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTACCATACTATGGAGAAATACAGTAATGAAGTGTGGCAGAACTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTGTCTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---			AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGCTGAGTACAAT ACATTTCATGTCAGGATAAGGAGCAT/GJACACCAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGGGAGGCGGGGTTGGTGGAA
WI-20270a	53 G A ---			AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/GJTCAGTGTAC AATACATTTCATGTCAGGATAAGGAGCATACACAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGGGAGGCGGGGTTGGTGGAA
WI-20622	130 T C ---			CCACTTCAATAATTTACAAATGCTCAGCAGCAAAATATGAAAAGCTTCAACACTTCCCTTTGTA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[TC] TACTAAATTTTATGATGTTACTCATATTTTATTCATATACTTTAATGACATCATTTGCCAATACATA CAATTTTCTNTAACTTTATTTTACAATAAGCCAACTCTGTCATGCAG
WI-20768b	190 C T ---			TTCCACTCAAACTCCCACTCCCTCTCTGGAAGGCGGGCTAACAGGACCTCTGCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATCTGCTGGGAC[CT]CAGGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---			TTCCACTCAAACTCCCACTCCCTCTCTGGAAGGCGGGCTAACAGGACCTCTGCTGCTGCTGC TCA[CT]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATCTGCTGGGACAGGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---			TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAATATCTCATCTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTGTTGGTCATCTTTAAAGAAA TGCTTAACATACCAAAG[AT]TAGTGGAAATCAATAGAATAAAATATTTAAGCTTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATTTATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---		TGTTGCTTTGGTTGTTGCTTTCTGGAAACATATTGGAACACTTGTGTTTTCATAAGCTGCTCAGAGT GGCACAAATCCCATCCATCTTCAGGCCCTTTTAATAAGGTCAATTATGAATCTGAATTTCT/GAGTTAAAT ACTCTGGTGCAATTCATTTCACTGCAAAAGCAACTGGCACAACTCCTGCGGGTGCAAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACTTCTCCAGCTCAC
WI-22189	70 C T ---	---		CCAAAGGATGAAATTTCCACATTTATTTNCTTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGGCATGGCGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---		GGGAGGCATCATAGAAAAAACCCTCAGCCAGAGTTAGGACATTGTGATTTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTCAGGCTCTGTTGT/GTCTATTTGCAAAATAAAACCCA GACCGGTGATCTTTCAAGTCCCTCCAGCTCTATTTATGATTGCTCTTAGTCTTTATGAGCCA TGATGATTTATCAGTCTCCCTGATGCACTCACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---		GACGTCACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGTGAGGACCTTGTCTTT CTTTTCCAATCTCTCTCTTAGCCAGAACTTTGCGAGAGCCCCCTTATTTCTCTTCCCTCTATTCC CCTCCTTCCCAATGTGCTAAGGTCCCAATCCAGACCCCTCCACG
WI-22292	53 A G ---	---		CCAGTGGAGGGTTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/GAGTGTGAGTAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---		ACCTTGCACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATCCCACTCTGGCTCTGAAG GCTTGTCAACCAAAATGGGAGCTGGGCTAAGGCATATTTAAACAAAGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCAGCAAGGAGGATTGTGGTCT/GCCTTGTGTTTCTG AACAGGGCCAGGGCAGCCAAAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---		GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTGAATATTT GTAGGATGGATGAATTTGAAGTGAATTAAGTCAAGATAAAGGGGCAACTCTTTAATTA/GAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---		TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAGTGTAAITTAGAGT AAATACATTTGGCTGTAAAGTCG/ACGATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---		CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNTGCGCTTCCAGGCACAGCCAGTGCCT /CCTGGATGGCATCAGCACAGGCTCCCTGCCCCGCGCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---		ATTTTCCCTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT/GTGGAA ATCTGCATGATTAATAACATTAAACAGTTTCATAAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATGCACATTCTCCTCCTAGTT T

WI-21763b	154 A G ---	---	CATACCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTTAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTG/CAGACACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCATT GA
WI-21763a	135 T C ---	---	CATACCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTTAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCATT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCAGTCGAGGTGCATTCTTCTTATCTTGTGTTAAGCCACTTGGGTA/A/CJ TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGTCCCTGGAGGGAGGCTTTCTTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/C/GAAAAAATACACAATGGGAACAGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCCTGGCTTTCTGCTCCAAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCC/A/GCCCCACAGGTTCTCTGTT TCCAAAGTCTGTGATTGAGGCAAGACCTTCACACATTCACCACTCTGCTGAGAGGAGGGTCTC ATGAGGCAGCCTGTGTGGTGGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAAG/C/GTGTCTATGATCAGAC CACCTOCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGAGGAGGAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGTTTAAAGGAGCCTGAGAAGAAATTCACAACCTATTGACTATACAGAG TCTTCAATTCACAAACAGTTAATAGTAAGTGGTGGCACAATACAACATGCATTGAATACTCTGTAT TATTCAAGTAAGTAA/T/C/AGGNTCCTGCATCATTCTCTTCAACA
WI-22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAATCCTTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGTAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATG[C/T] GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	88 G A ---	---	ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAATCCTTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTG/A/ATAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATG GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCAAACACCTCCAGGCCACCCCTGGGGCCAGACACCTCATGCCAGCAGCAC CTACGTGGCCGAGTACGGACCCGCTGGCCCAAGTTCTCGGCTCTCAGACGTCGCCAGCAAGTGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCAACCTG[C/C/AGTGGCTTC TTTGACGGGGCCGCGCTCAGCTCTCTGGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	CT	---			GCAGCCATCTCTCTCCAAACCTCCAGGCCACCTGGGGCCAGAGCACCTCATGCCCCAGCAGCACCTACGTGGCCGAGTAGGACCCGCTGGCCCCAGGTTCTGGGCTCTCAGGACGTCCAGCAAGTGGA
						GCCAGAGGTTTG[C/T]TGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTTC
						TTTGACGGGGCCGCGTGCTCAGCTGCTCTGCTGGAGGTGAGGAAGGAGGT
siFIBBb	412	GC	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGGCTGAGCAGCTGTGATTGTGCCA
						CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCTCTCTCTGATCATGCCAGG
						TTTGACCCAGCCTCGAGTCTCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGA
						AGGACCAAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siFIBBa	341	TC	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGGCTGAGCAGCTGTGATTGTGCCA
						CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCTCTCTCTGATCATGCCAGG
						TTTGACCCAGCCTCGAGTCTCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGA
						AGGACCAAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siGLV2	61	TC	---			GTCAAGAGGACGCGCTCTGGGACGTCTCCACCATGGCTGGGCTCTGCTGCTCTCACTTCCTC
						CTCACTCAGGACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGCTC
						TCCTGCTCTCAGGCTCACCGGGGCCAGCACTGACTCACTGGCATGT
siSG1001	70	TC	---			GTTACGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGGAT
						TATTC/JAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT
						TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
siSG1001	33	GA	---			GTTACGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGG
						GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT
						TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
siSG1002	63	AT	---			TAATGATAATTAGGCATTCTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGC[J/T]
						AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
siSG1009	36	GC	---			GTGGAGAAAGATCGTCTTTCTCTCCCTCCCATGACCG[C/G]GGCTTCCCGGGCACCTGTGCGTTTCC
						ACCCGAGACGGCCTTTGTAGGGACCCACTGCCCCACTCGCTGCTGTGCGCTGGGTTCCGCTCTAG
						GGCTCGAGTGTTAAG
siSG1011	107	CA	---			TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGGCTGAGGGCAGTACCCCTCCATTGGGC
						ACAGTCCAGACCCCAAGTCAAGATGCCCATCTCTGGG[C/A]CTCAGCCCTCAGTTCTTCATTCC
						ACCAGGCCGTGCTTGTGAGTTTTCTCTCCAGTGAG
siSG1012	89	TC	---			TAGTAGGTAAGAAAGCAAGGAGGATTGCTTATCGGATGACTGTTTACAGTGGTGTGAGACTATGC
						CGTGTTCACGAACACTTAAATAT[C/G]GTGTGTGTAATCTGATTTATCCTCGTCTTACAAATG
siSG1017	42	CT	---			TTGAAGCAATATTGTCTAGCAGTCTGCTGGACATTAAGTCCG[C/T]GGGAGGAGGAAGTGAACAGGAA
						TCGATTCTTTGTCTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC

stSG1019	3	136 GA ---	---	GGAACTACTACCTAAGGACAAAATACTATTATTAACAAAAAGTCTTCTAGTGTATATTGTGTAACACATTTCTGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACTTTTAC
stSG1020	2c	143 GT ---	---	TG/AJTTGAAAACCTGAGATTAAAGTTGCAAACT AAGCTAACTTAGTGAATGGTGCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCTGGCTTGGCGAGAGTCAGCCTTGGTCACTCAACGGGCTCCAAGCTAAGCGGTCAAGGAAGCAGTCCCACTGCTTCTOGCTGTCA/GTJCAAGACCAAGGCAGATGCCCACTGCTCTCTTCTCTGCTACTTCT
stSG1020	9b	75 AG ---	---	TCCTTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAATCTCTTAAAGATCCCACCTTTATTTTTA/GCTCCAAATAATGTAATTATCAGCTGCTGAATT
stSG1020	9a	34 CT ---	---	TCCTTTTCTCTTTTCACTCTCAGTCACCATGATTCT/AAATAAACTAATCTCTCTTAAAGATCCCACCTTTATTTTTAACTCCAAATAATGTAATTATCAGCTGCTGAATT
stSG1021	8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACA/TCTGTAATATTTAAAGAAGTTATATTGTTTGACATAAATGCAATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025	2	108 AC ---	---	ATAGGTTTCAGGAACAAAATCAATAAATGGAAAAATGAGAAGAAATCTTTATTTTTGGACCAATTTT AGGCACCTTAAGAGTTTTCTTTCTCTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915	0	123 AC ---	---	CTGTATTAATTAAGAAGGCACCTATTAAATGAGGGACGGAATACTACCTGTACACAAAATCTGTAC TTTAACAGCATCTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/CJATTTTAA GAACTGAGTATTGGAC
EST11023	1	166 TA ---	---	TTTTTTGTTAAACCAACCCTGAAAGTTTCCACATGTGAAATATAGATACAACAGTGAACAAAAT ATGTGGCTCCCATGTACATTGGTTACCTATGTACAAGTATCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAAAAAAATAGTACATGTTAT/TJAGTGTAAATAAAATTAATTTTACAAAGGCTTT TCCACTCGTGGATTGATCTCTTTTGGAGGGAGTAACTCTGG
EST14096	8	71 GC ---	---	GGGATGTATATTACAGATAACACAACATCACAATAATACCATCAGACATTGAAAACTAAGGCCATCT GTGA/GCTTATTTTAAACTGGTGTGTCACATAATGATCTTAAAAAAAATGAATTAACCAA ACCAAGATTCTCTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113	6c	125 CA ---	---	TGCAATTTGTAGAAGGCAGGCGGCAACCCCTGGGACCTATCTCTGTAGAAATGTGAGGTG CAGGGATGCTTAAGTCTCTCTGCGAGAGACCGAGGTGCAGAGATGATCTTCTCA/CJACCTTC TCTCAGGTCGTGGAG
EST22555	7	60 GA ---	---	TCAAGCATGTGTAAAGGCAGTCCCCCGCCAGACCTTCTAATCTTGCACACTGGAAGGT/GA/AAA CCTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGCACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCGGCTCAGAG

EST22917 6	74 C T ---	---	GTAAACCTTGCAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGGCTCTTGGGCTCTCAATGCA ATAGAAAC[CT]TGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCTACTCA[AT] GTTGTGGTTTGTAGCTCAGCTGCACACAGGAAGCTTGGAAATTTGGAGGCTCCCAAGTCACTCTCCA GAGGGGAACTTCAAAGAGGATTCCAAACAGTGAAGCAGAAATCATGGGGCAAAAGTCA[AT]GTATGG GGCAGAGCTGAGTTGGACACACAAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCGCG ACAGCAGGAGTAGCCAT
EST36745 3	56 A G ---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGTATG TJA/TJATTGTGAGTGGTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATG/TJTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCA[CT]TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	TATCGTGGGAAGTTCCAACTCATCTACTTATGCTGCTTTTCTACTGCTAATATTGGATGCTTCTTGCCA GGCTC[CT]TTTAAATTGTGCTGAACCTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA
STS- R42778	74 C T ---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCTCCCGGATGGTGAAATGTTCCGGACCTAGATA[CT]GTGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAAATTGTTCTTCTGTT[CT]GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
siSG1026 6	55 T C ---	---	GTATAATTGAGCATAGCCAAAGCCTTTTAAAAAACCATACTATCATTTTATGAAATCTTTTACA AGA/T/GAAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---	---	CACCTTAGATATGAGGAAAATGTTTAAATGGACACAAAGGAGTCAAGCAGCTTGGAAACCAACATAG TTTCATACCACGTTGAACCATGTGTTTGTATGCAAAATACAGCAAAATATTTTTCACCT[CT]ATG TCAATGCCAATGCATTGAAGGCCCCAGAAAATGAGAAAAGGATAACAAAACCTTTTGTATAAAAAAGGTA AGAATTTCTGTGTG
siSG1031 0	128 C A ---	---	

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGGATGCAATTCGG GCTCCAAACCTGTCTAGGAAGGCCTAGACCTCAAACACACCTCCATTCGCAATTCCTCTTTGG CTACTATGCTTTTCCCTGACTCTGCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGGATGCAATTCGG GCTCCAAACCTGTCTAGGAAGGCCTAGACCTCAAACACCAATTCACCTCCATGCTCTCTTTGG CTACTATGCTTTTCCCTGACTCTGCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAATGGTTTATAAATCCTCCTCTTG AAATTATGTTACGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGT
stSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACAGTGTGCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGTCATAAATGGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACAGTGTGCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGTCATAAATGGGGCAA
stSG1385 b	117 T G ---	---	TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGAGGGTTGAGGAGCGAGAGGCAATTTT TGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTTGTCATCAATTAAGAA GACAAAGGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGCTCTTAAACATGAGCC CCAGCAGCTTCAGTCCCTTCTGCTCG
stSG139	69 T C ---	---	TCGTCTCTTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTGTGTCT TTCGCTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCTGCCACTGATTGTTACTGCTTGTGCTGCTG GATCTGGTTCAGACAAGGCTGATTCAGAGACTCCACGCTGGTCAAGGCTCTGTTTGTCAATCCCT TGGCTCTCCACTTCCAGTTGGCTTCTGCTCCTCATTCAGTCTCTCCATGTGGCAACCAAGATGGC TACTGGTGGTCCAGGTTACGCTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTAGGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCJTTTAAATCAAGGTTGAGA ATGACGAATTCAGAAATTTCTTTCATACATAAATGCTTCTCTAGTCTGCAAGATGGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA TCGTAATGTGGAGGATGCTGTTGACGCTGTAGTTACTAATGACAGGAAACCCCAATGCAAGAGGAA AATGCCTGA
stSG1696	67 C G ---	---	

stSG1847 b	95 GA ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTACCCCTAAATGAAAGAAATTT AGAGGTTAAATAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATGACTGTGCT TCAACACAACTG
stSG1847 a	49 CA ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTAC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATGACTGTGCTG TTCAACACAACCTG
stSG1897 a	83 AG ---			CTTAATGCCCTTCCCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACT[G/G]GCCACACCTTCTCCTCCGGTCTCCCAAGATGACT
stSG2022 a	86 TC ---			TGCTTGAGGTTTCAAACTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT[C/A]ATTCCATAATCTCATCTATTTAACATTAAACAGGCCCTTTGTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 CG ---			AAACGTTGCCAAAATGTGTTGAGTTTCAAGATATAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACTTAAGAATATATTTGACATT[C/G]ACATCAGATGGGGCATTTT
stSG2108 c	71 AG ---			TTGAGCAACAATGATTCGGAATTTGGCAGCTCCAAACCACAAAATGATTGAGGGCTCCACAGAGA GAG[C/G]TTAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 TC ---			TTGAGCAACAATGATTCGGAATTTGGCAGCTCCAAACCACAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 AG ---			TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAATGACTGCGTGTAC TGAATCTGACTGTGTAATAATCTCAGAATGGCAGCACCACCTGGCATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[G/A]AGTTCCCTATTATATATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGCTCTG
stSG2141 a	113 CT ---			TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAATGACTGCGTGTAC TGAATCTGACTGTGTAATAATCTCAGAATGGCAGCACCACCTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTTCCCTATTATATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGCTCTG



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stSG2148	50 A G ---	---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTCAG/AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGCAGGCTC ATCAC
stSG2175	68 C T ---	---	---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGAAGGGAGTGAAGGACCA
stSG2189	41 C T ---	---	---	CAAGTGTGAAAGCTGGGATTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTGTATAGGTTATCTCAATCCTACTC CAGCTTGGGAAC
stSG2200	49 T C ---	---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGTTCTGTATGATG/T[C/T]TATATTATGTAT AATGTCCTACCTGATGATACCCAACATATTACTAGCCTTATAGATGAGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	---	CATTTCTGCCTCCTGCTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAACTCTGTAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTCAGGAAGTCTCGCCAAAGCACTGGGCTGCTCTCAGGCAAGATTTCTCCT
stSG2306	67 A G ---	---	---	GTCAACGCTGAGAGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACTATTTTACA [A/G]ATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	---	GAAACTACCCACAGCATGTATAAAGAGAGAGATGAAAGAAATAATCCCGCAAAAAACA AAAAA[T/G]TGCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63 T C ---	---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGTCAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGIGTCTATTCTGGCTGTGCTTCTATTTCATCA
stSG2465	76 C T ---	---	---	CAAGACTAAGAACCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	---	TTGCAGGCTTGATTCCACAATAACAAGTCATGTATAGAGAATGTGAAATGATACITGAAACCAA GATATATAAAATATTGAAGTCATTTATGCCCTTTGATGACTGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	---	AATTGCCAAATGGAAATTCOCAGAGGATTTTAGACCAACTTTGCCCTGTGTCATTCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATC CCGGCCCCAGATTATTAAT

[illegible]

siSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTATTTATAAGGAA[TC]GCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTCAGCCACATTCAAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTTCAGTACATGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTGTGACGTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141 C T ---			TGTACTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGACTGCTCTTCCAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACOCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[CT]TGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3269 a	24 A G ---			TGTACTACTGTGTCATCCTATCC[CA]GTTCCCTCCCTGAGCCTGGACTGCTCTTCCAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACOCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3284	130 C T ---			TAACTCAAGAACCTTTCAGTTACAGGAAGATTATCTAATATAAATGACTAAATACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCA[CT] TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTTGTTTGTATCTACCC
siSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA[AT]TACAAATCAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTAGCTCTCACT[CA]CCAGTGTATCCATTTCCCGAGCGGTAGAGCTTTCTG TTTCTGTAGATTGCCTGCTCGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTGCTTCATTCCTTTAA
siSG3369	69 C T ---			GATCCCCAGTATTATTTCTAAATTGAACCTGTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG[CT]ATAAGGGAAACCCCTCTTTGCTTAGTTTCTAAGGACTTTCT
siSG3398	125 G T ---			CAAGACTGTAAGAACGTAGGCCTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACTTTGTAGC[GT]CTGGGT CAAAGTCTAAGAGGACAAATAATAGAGACT
siSG3416 a	43 A G ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATACG[CA]GCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTCCACCTCAGCCAACTGAGTAGTGGCCTGCAGGACAAAGTCAACATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3424	173 T A ---			GTAAGACAAGGTTTGTATGTTGACCAGGCTGGTCTTGAACCTCTTGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGAGCCACTGCCCCCGGAGCTTTTAACTGAAT GTTGAAATCATCTGCTCTTTGCTGGGTAACACTGAT[CA]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCCCTTATCTGTAACAAATGGAACACAGAACTTTTCCCTTCTCTC
siSG3436	88 T A ---			GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGTGAGGCGCCTCACAGA ATGAGTGGCAGAGGGGCCCTT[CA]GAAATAGCTTACTCTGTTTCTCTATC

stSG3463	103 C T ---	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTGAAGGACAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTAC[C]TJTGGAACAACTTGCTTGACTATATTA CTGA
stSG3491 b	71 G A ---	---	CAAGATACTTCATTGCTCTAAGTAGTGCAGTGTGGCAATAATTTCTCAGCAACAGGACGATTTG AAGA[G]AGTGGAAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTTCTATTAACCTCATTTATCTTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTTT[C]TGCAATATATGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCTACCTACACAGCTGTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGTCTGAAACGCATCTCAGTGTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTAAG[G]GTTCTGCTGGGTGTTCTCAGTCTTGCCATGGAATG
stSG3583	112 G A ---	---	GAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTGGAACCTGCGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G]A/JTACATACACAGTACTGT CTAGTTATCAACACTAC
stSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTGCTCTACTAAAAATTTAAAAATCAGGTGTGGTGG[G]C/JACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101 T C ---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACCCCTGGCACAAAAAACCCCAATGA[T]C/CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAAACAACAAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTCTAAAAAAA AAA[T]TTTCTCTGATGTCTGTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTGCAGCTTAAATTTCTTGAATTCATACGCT TCTGTCA[T]T[C]A/CACAAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAACCTGCCATTAGTACCATATTTAGGATGAGAT[C]JGGATTGAGAGGCATGAACCAAGG ATCGGTAATAATCATTTATGAATAATAAGTTATCTGGGAAACGGCCATTGTGCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTGGCAAGAATATATGATGATAACAATAATATGCTTACT GGT[G]A/JATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCAIT CTTCTCTTTGTA

siSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATGATGATAACAATAA/GJ/TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATG/AJ/TGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCTGGACTCACCT GAAATATCCTACGAGGCA/CJTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGGAAAAAGG
siSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC/CJ/TCTGAAAGCCGATGACCATCCAACCTGGACTCA CCTGAAATATCCTACGAGGCA/CJTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGGAAAAAGG
siSG3698 b	145 G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCAACCAATCCCAAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]GAAATACCCACCCACCTTCCCTCACTGCAGA
siSG3698 a	51 C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCAACCAATCCCAAGGTTG/CJ/GJCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGTTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGTGAAG[C/J]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
siSG3725	104 G A ---	---	GCCAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATACCAGCCAACAGCAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
siSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCACTACCTTTTGTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGGAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]JTT GCTGACTCCTATGTGTTCAAGAG
siSG3787	49 T A ---	---	TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAAATAAGGAGTGTAGGCTAAAGCAGTATCTTCCCCT
siSG3880 b	115 G C ---	---	GACAAGAGGGGAAGAGATGGCCAGAGACCAAGGCTGGGGCTGGGGGTTCCCTGAGTCCAGGGGC CACCACAGTCTCTGTGGGTCAAGGCCCTCTCTCTGGGAGCAGGTCTA/GC/JGGCAGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTTGCCCT

siSG3880 a	36 GC ---				GACAAAGGGAAGAGATGGCCAGAGACCAGGGCTG[C]GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGCTAGGGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGACCCCAAAGAGTCCATTCTGCGCT
siSG3895	44 A G ---				AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[C]A/GTJTJTJTJTJTJTJTJTJTJTJT TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGAACAAGATGCTGATTCGTCAACTG AAAAAT
siSG3902	104 T C ---				TCGTGTGAGACTGGAGAGACCAGGTAACCAAGCACCAGCTCTGGTGGGAACCTGGCTTCCCTGATAACA TCATCTATTTCACTAAATGTGAAGTCTTCTTTCTT[C]T/CAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTGTCTGGACAAT
siSG3935	50 G A ---				GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[C]G/AJCTAGTGTGCAGGC TCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCTGGACGT
siSG40	25 A G ---				GAGGAAGAGGTTGAAGAAGTCTGA/GA/AAATATATTTAAGATTTCTTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAATAAACCCCTTGTGTATGTATCA CCCAA
siSG4009	32 A G ---				GTGTGGGTGTCTGATGATGAATGGCGGCT[C]A/GTACTCTTTACGGTCTTACACTTTTATGTCCTCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTTCACACTGCTTACA
siSG4033	123 T C ---				AGAAGCCTTGGGGACAATGGCAGTGCCTTCTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTCAAGCATAAAGGTACTTTT[C]TGTGAAC AGGTGGGCAACAC
siSG4038 a	29 G A ---				GCTGAGAGCACGTGTACAGCCAGCCTGT[G]A/CGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTCCGGCTCCGGAGAGCAGCTGAGGGTTCCATCACT
siSG406	53 T C ---				ACTGTGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAT[C]G/GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTCTCTAACAGAGATTATTAACCTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55 GT ---				ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGTAGATGTATTAG[C]TATAAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGIGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4095 a	27 A C ---				ATCTGGGCTGAATTAGTCAAGCAGGTC[C]A/C]GATACTATTGTCTGTAGATGTATTAGGATAAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGIGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4120	65 G A ---				TGCATGTTCCACATCTTTTATAACAGCAAAATGTATAATAAATTAACGTACTTATGGATAATCAC[C]G/ A/C]TTTTCCCTCAGAGAGCCACAGTTAAACAGCTTCCAGCACACCATTAATCCACCGAGCT

siSG4128	54 A G ---	---	CTTGGCAGATAAGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTTGTATATATTT TACTTCTTGAAATGCGACATAATTTGCAATAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAATGCAAATGTTCCAGAGGG
siSG4209 b	128 GA ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCGCGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGCGCGCACTCCCTC[G]A/GC AGGGGACCACGAGGCGACAGGTCTTTGATGCTCCGAAAGCTGAGCTCCATTCCA
siSG4209 a	65 GA ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A/CAGGGCGCGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCGCGCACTCCCTCGGC AGGGGACCACGAGGCGACAGGTCTTTGATGCTCCGAAAGCTGAGCTCCATTCCA
siSG4254 b	31 GA ---	---	CATTACCCAGAACGCCATGGAGGACCAGAGC[G]A/CACGGCGCGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGGTGCCTCTCCCCCAGGGGCGAGCGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCATG
siSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAATAAATTT/GIAGCTTCTGAGTAGTTGTTCCAGTTTCACCCAAACATTTTG
siSG4331 b	71 T G ---	---	CTCACAAGGCCAACACAGAAAAGATACAAATACATTATCCAGCTAATATTAGTTTATGACAC AGAGT/GITTTCAAACAAGTTTAAGTGCACCTGAAGAGCATGTTAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTTCTTGGCTCGCCCTTGATCTGTTTGAGGGGTGTC
siSG4340	76 GA ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAACC ACATGTTCTC[G]A/TAAGTGGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC/CJ/CCTTCACAACACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
siSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
siSG4376	73 A G ---	---	TTTCACTGCTACTGTTTCGGTGTCTGAGTCTCAAACCTGCTTTCGAAGTGTCTTCCAAAGGGGAG AACAG/GJCTGGAACCTCGGCTCTGCAAGAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
siSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTT/CJ/CAGTCTTTGTAGT ATCCACAGTAGTGTCTGTCCTATGTAAGTGTCTGCCAGAACCCCAATTAAATCCATGCC
siSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTCATCCGATATTTTGGCCGATCTGAATACTGCAAGGGCTTAACCAT TCAAAACACCG[G]A/GJTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65 C T ---			AGCAGATCAGTCAGCCACTTGTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA(CI TGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGAGGAGGAATAGGCAC AAATGGAATCTATCTGCTGCTCTCTCAGGTC
stSG4430 a	54 A G ---			ATGCACATTAAATGAATGGCCTAACTACTGGAACCTTTAGTAGTTCTATAAGGTA/GIATTAACATA GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCGCCACCCAGGCTCT CGCTAGCCCTGCCCTCTGGGTCAGTGC(G/ATGGGTTAGGCCCCCAAAAA
stSG4448	99 G A ---			ATTAGCCATTCACTTGAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT TAACTTTGGACAACCTAAACCTTA(T/C)TAGTGACATTGCTGTCTAATAATCAAAATACTTCATCATA GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
stSG4449	92 T C ---			CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCTCA(CI/A)GATGATGTCCATGTTTGTGT GAATGAAACTCAACACTCTTCAGTTTTAGAGTCATTTTCTGGTATCGAGCGACACACCGGAGGAG CACACCCTGCTCCAAAGGCTGCTGCCCTCTGACACAGT
stSG4467	42 C A ---			ACATGTCATTTCTGACCAGG(NC)ATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA TTAAGAGACACAACACTGGACTTTGTTTCTTTACTGTAGCACCCAGGTTTCATG
stSG4475	21 A C ---			GTAACATTTCTGGGGTGGGGTGAGACAAAC(A/GIATGAACCAATAATTAATTACAATTATACATT TCAAGGAGACTTTTAACTAGGTTAATGTGAACCGCAGCCATCAATGTTTGTGAGGAAAGGGAGA TGAAGTCTGCTGTGGGGCAACGTTTGGCCTCATTCGAGTCAGACTGGC
stSG4477	32 A G ---			TGAACTCAGAGCTGGGTGGGAGCTCAGCGAGGGAGGCTGGGGCCAGATGAGCCGCCGGGA CAGCAGGCTCG(CI/GCCACGTCTGCGTTGTGAAGAGGACATAGGCTGCCCTGGACTCGATCT GATTCATTGACAGGGGAGACGCTGTTGTCA
stSG4531	79 C T ---			TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGTAGGAGACAGAGTCTATT AAAAGAGACAGTGGGCACC(GI/A)CAATTGGAGGGGAAGCGGGGCGAGGTTTATAGAGAAC
stSG4550 b	86 G A ---			TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGTAGGAGACAGAGTCTATT AAAAGAGACAGTGGGCAC(CI/G)CAATTGGAGGGGAAGCGGGGCGAGGTTTATAGAGAAC
stSG4550 a	85 C G ---			AATCAGGCACAAGCTCGGGAGAGAGCAACAAAGCTCTTCTGCACI(GIATGGGAGGGAGACAC CATTGAAAAGGCATCGTTCCTTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
stSG4590	47 A G ---			AACTGTATCACCCAGCGGT(GI/C)CAATGTACTAGTACTGTTCCACAGGGATTTTATACTATTC CTATAAGGTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTATCT TAATATCCTGTTCAAGATGCTCTGGAG
stSG4623	22 T C ---			TAAAAAAAACAACCCCCCAAAAAACCCAGAGTTTGTAGTTTATGTTTTCAGATTTAAAG GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCAI(AIATCAGAAAAGTCTTCCCTACTCCAAAGTGA GAAAGGA
stSG4843	102 A C ---			



stSG4850 a	38 CT ---	---	GGATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC/TGTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGTGCTGTGGGGAGGTTTCCAAGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGAATCTTGGGTCCC
stSG4879	86 AG ---	---	AACCTTCC AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGTCTCTCTTTGCAGAAATGGCCTG CCCCTGGAGCTGGAGCAG/AGTCTGGGTGAGCTCTAGGTGAGGGTGGTGGAGGGGCATAGAAAT
stSG4885	104 GA ---	---	AACTTCC ACTGGAGTGGCTGCTTGTGAGCCGGCTGAGCGGCTGGGACTCGCGCTGACCACTCGCTCTTCAG AGACTCGCCCGCGGTGACCACTACGCTCTGCC/G/AGTGGGAAAGCAGAGCAGGACC
stSG4896	112 CT ---	---	AAACAAATCAAAACCAATCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGTGGGGCTGGGCACTTTCT/TC/AGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 GA ---	---	ACAGTCCGATGGTTACACAA/AG/TTGTAATGTATTAATCCCACTTACGAATGATTAATGA TAAATCTTATGTTTATTTATCATCACTACCAAAAGGCTGGGTGAGGGTGTCTTCTGTCCT
stSG4950	24 AG ---	---	TCATGACTCCAGGAAAGGTCCT/AGTCTTAGCTTCTCCTCCCTACTTTCTCTACATGTCAGC ACTGTAATGTAGCTAAGATATAGGCAATGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 GA ---	---	AGATACGGGCAAAACACTGGATGGCTTCTGACAACTTAAGAGGTCTCCGAGTTATATCTGGGT GGGAACACTGACCCAGCCCTTATTCCTTCAAGGACTGTAGTCATTTGGCAAGGAGGATTCATGAGCC CC/G/AGTGCACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 CT ---	---	GAAGGTCTCTGAGGAGGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TTAGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 AG ---	---	ACTGGTCCCTCTCAGCAGATTCAGGGGTGTCAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGCT/AG/TTACCCCGGAGCTAGACAGCCCTGGGTTGAATCTCAACTTCTCCCTTTCTTGTGTGC AACCTTG
stSG4997	22 TC ---	---	CAAAGGAGTAGGAGCCCCAA/TC/TTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 CT ---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAACA/C/TTATGCCATCGCGGAAATAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAAGAC
stSG6345 a	107 GA ---	---	GCCTCTGGTCAAGCAAAATTCCTCAGGACAGCAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAATGTGATGTTTGTCCAC/G/ATAGTTCAAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG



stSG8145	97	CT	---	---	TTGTGGACTTCAAATCTTTCCCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCCTGTGCTGTGAAGG
a					ATTGTTCTTGCAATTGCTTGGATTTTTCAGAAATGTAAGATAAATAACACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8150	36	A	G	---	AGAGGATTATGGAGAGAGCTGGGCAGGATC[T]CAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAAACGCTCATCAAAA
stSG8340	30	CT	---	---	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGATTTTGCACTACCT[G/A]TGAAGCAGCACACGACATTAT TTGAAAG
stSG8466	111	GA	---	---	GATCAAGCAGTGCACACGGGTACAGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCGTCTCCCTCGTCGGGGGCCAACCCCGCTTCCATGA GGCATTGGGGACGTGCTGGCGCTCTCGGCTCTCCACTCTGCAACATCTGCACAAAAATCGGCCCTGC
ESTD-ACE	--	--	--	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTTCCTTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCTCGGCACCTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGCTTGTGCTC
ESTD-ADA	--	--	--	---	GGGAGTGACAGCTAGACACCAAGGGGGGCTCTACAGCTGTGTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-AK-168	--	--	--	---	AATCCAGCACCTTTAGGAGGCTGAGGCAGGCATATCACCAGAGGTGAGGATTTGAGACCAGTCTGA CCAACATGTTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCGAAGTTGTGTGAGAGCCGAGAT GGCAACATTGCACTCCAGCCTCGGCAACAAAGATAAACTCTGTCTC
ESTD-ALB	--	--	--	---	TCTCCTGTCAATTCCTACTCCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGGACTGCCAACTCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-ANT1	--	--	--	---	CCAGGTGTTGTGGCAGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAACTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAAGTGAATCGCGCACTGCACCTCAGCTAGGTGACAGAGCAAG ACTCC
ESTD-APOA2	--	--	--	---	GGAAGAAATGGAGCCTGTGGGAAGGAGGCGTCGAGGGGTGGCTTTGTGGCAAGCCCTTCTCTGA AGCAGAAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATAATTGACCCAAAC
ESTD-ARSB	--	--	--	---	

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAAGGTGGAGGAATTTGAAAGGECATTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGAGGCGGCCCTAGCCGGGGCCCTGCTGCGCTGGCGGTCTGCGCAOC GTGGAGGCAACCTGCTGTGTCATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTGTGACTTGGCTGGCCGACGCGACCTGGTGTGATGGGACTCTGTTGGTGGCGCGCGGCCACCTT GGCC
ESTD- BA511	--	--	--	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGTTGCCACTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTAACTCCTCTCTCTGGGGCCGTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGTACGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAGCTGTCCGAGAGGGCTACGAGTGGGATGCGGGAGATGTGG GGCGCGCCCCCGGGGGCGCCCCCGCACCGGCATCTTCTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTGAGAAACCCATAGAGCCCCGGAGACTCATCATCTCGGCAAGA GACCAAGAGGTGAGCTTCTGTTGCCGGGAAAGGGAGGCGAGGTGACAACTGCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGGCTGCCATCTGCCCTGGCACA
ESTD- BRCA1a	--	--	--	---	---	AAGAAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCTAGAAAGAGAACTTATCTAGTAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCTCTCCCTAATTTGCTCCGGGAAGCACATTCATCAA CCAGTCAAGTTGGGGGACAGCCATGACATGAGCCTCTGTGAGCCTTTCACCAATGATTCATCTAA
ESTD-C8	--	--	--	---	---	GCTCTGCAAAAT

ESTD-C7						ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22						GGCAAGTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACTGGAATGTTAG GCAGTGCTTAAGTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGTTGCTCTTCCCGGCTTCTCTCACACAC
ESTD-CB23						TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGTGCTTTCCCGGCTTCTCTCACACATACACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCACCCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24						ACCAGGACAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCGACACGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGCCCGAGCCCTCAAGGAG
ESTD-CB25						GTTCCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTGGCCGTC TCTGCTCTCGAACCCAGGGCATGGAGAAATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTGCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTGTCTGCCACC ATCCTCTATGAGATCTTGTAGGGAAGGCCAOCCTGTATGCGGTG
ESTD-CB27						TTTTCTGTTCCCTGAAGATTGAGTCCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTTGGGCTGGTTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TCTCCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c						AGAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTGTCAGTTTCAGGGTGTCAAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGTAAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d						TGAGAGAACACCTAGTCTCCATCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACTGGACTTCTTCTACTGACGAGACAAGACTTACCC AAGAGAGATTATGGCAAAGATATACAATAACAATTTTATTGACCAACACTATCATATGGAACAGC ATT
ESTD-CPT2						GCCGCAATGCCGGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTGCTTAGAA GGCAATCCATCAAAAGTTAACTCTGGGCAGATGAAAGCTACCATCACTTCTCATCATGAAAGC TGGAGGCGGGCATAGTGTGCTATGCCGTATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTGGCTGGATTTCAGCGGCACAAGGCTCAGOTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGGAGGATGCCAGCTTTGTGTGTAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGCCAGCGTGGTGCAGGTTGTCACCATCCCGGAGAGAACAGTGTCAGCCACCACTATGCACAGGT TCTCATCATGAAGCTGCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTAACACCTTTTCAATCATATACACCAATAAATTCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCAATACTGATTAAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGCCGT CATGCTGCACACATCCAGGGGCGCCTACCTTTGTAGTCCATGGGAAAGCTCCTCTGGGGCGGTG GGGTGTGGTGTATGTGGTGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTTGCGTTATT GCAGATTGCTTTGCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCCAACATGGGAAATACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGAGAGCTTGCACTGAGTGAAGCAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAAATAAGAAATTAACAGAAATATCATTTGT TTATCAAACATTTATCACTTATTTATTGGTAAGCCATAGTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTAATTTTCAAAAACCTCTCTACAGCCGTTGTGTTAATTAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAATATGGTCAGGTTACAGCTGTTATCCC AGAAGTGAACATACCTGCTCTAGAGCCAGAGTACATGATGTTCTGTTTCGGTCTTACGATGG CAGGTATGAATATAATACTGTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGTATTT CTTAACAATAAATCTGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGAAATAATGTTATTT TAGCTGTGAGAAACAATACTAATCTTGATATGTTTCATGAGCCCTTGGGTGACCAAGGTGTAAT GCCAATAAGCAGTAATTTTGGAGGGAATCTTGTCTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCAGATAGGCTTCTCTACTAATACAGAAATTTTGAGAGAGCAAAACAACCTTCAAGG ATAATGGGCAATCACTTCTTCTTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAATGTATAAATCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTTTTACAAACATTTTCATCCATGGACTCCATACATAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	--	--	---	---	---	GTGGGACACCGAGGGCTCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGGAGGAGACA GAATGCTGATTATCTGGTGAGAACAGAACTTCTGGCTGTGGTAGGGGCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	--	--	---	---	---	TCCCAGCCTATCGGTCAATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAG ACAAACGGTCAGCACCCCACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	--	---	---	---	TCTGCCCTTGTGAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTAGAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCGACCCCG TCCACCCAGGTCTCCACAGCACTCCGACAGCCCGCCAAACCCAGAGAATGGGCATGCCAAAG ACCACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATTGCCCAATG
ESTD- DRD3	--	--	--	--	---	---	---	AAGCAGTGGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGTAGGAGTGTGGCGGGCCTGGCTGG CACCTGTGGAGTCTCTGCCCCACAGGTGTAGTTAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCAGAGGAGGTGCGTGATGCCAAGGGCTTCCCTGTGAGGAGA
ESTD- ERB2	--	--	--	--	---	---	---	TCTTCAGGATCCGATCTGCGCTGGTTGGCATCGCTCCGCTAGTGTGACGGCTCCACCAGCTGG GGTAGGGGTGGTGGTCACTGCGCGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCAACC CGCCTCACTCCGTTCTCTGCAGCAGTCTCCGCATCGTACT
ESTD- ETS2	--	--	--	--	---	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCACAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACACAG AGACTATTTTAGATTTCTTTTGCTTTTGCAACAGGAACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCAATTCAGAAGTTAGTTG
ESTD-F2	--	--	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCCTAGTAGCCCCACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAAGGCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCC AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	--	---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- G0DH	--	--	---	---	CGCAGACCGGTCA GTGTGGGGTGGGAGTGTGAGGGAAGGAGGAGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGGTGCACCGTGTGTCTGCTGCCCTGTTCAAGTGTCTGTCTGCTGCCGACGTGCA CTCTGTCCCGGAATTCGAGAGCT
ESTD-GCK	--	--	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACCCCTGCTGAGGCCACTCTCTGGTCAACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAATGCCAGCGCGCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCAACC TGCAGCCTAATTACTCAAAAGCTGTCCCGAGGTCACAG
ESTD- GNAT2	--	--	---	---	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACACAGGCATCATTTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	---	---	AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTTACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	---	---	CTGGGCTGCCCCGACGAGCTGCTGGCACTGGACGGCGGCCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	---	---	TTGGAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCCTGGGCCACACATTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCTCACAAAGCTATGATAACCTTAATTACCCCTGAGCAAAAGAGTTCGGCCTCCGGCTTGATTC AGATGGAGCTTTCCTTATCCCTGATGATGGATTGGTTCCTCTGCTG
ESTD-HT2	--	--	---	---	GGGCTAAATTTCCGAGCAACTTGCATAGACTGTTTATTGACTTGACAGGATGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAGACACACCTT
ESTD-HT4	--	--	---	---	ACCAACGAGCCCGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTGGTGCTTCTATCGCAAGAATCGTACTTATTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGACGAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	---	AACACAGAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGCCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTGGTTTCTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- GFBP1	--	--	---	---	ACCCAGTGGAGCCCGCTCATTCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC



ESTD- IGHV4-8	--	--	--	---	---	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTGAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAAGTGAAGT ATGTAATACTTCAAAAATACTAATAACGGAGTTGAATATAAAACCCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTTTATTTTGTG AGATGGAGTGTGGCTGTGACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTATGCCATTCTCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCGGCTAATTTTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTCTACCTGGGTGCTGTTCTCGCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAAGTCTGTAAGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCCTAGCCCGTGGGAAGCAGGAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCCCGTCTCAGGTTTACCACGTCACAACTTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTAAACCGTAGCAAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACAGGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTGTGCCTGTCTGCTGCCTGCA AGGGTTTGTCTAATCTCAATTCATGTCTCTTCTCATCTTTAGCAGCTGTGGGTTTGTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTATTAAAAATTTTTCACCTG
ESTD-MOC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAAGGTTTGGTCTAAGTGTCTAAGTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAATAATACCAGATCCACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	AACATGGACTTGTATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAGGGTGACTATTATCCACACTGCACACTGCCTAGCCCAAAACGCTCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAATCTGAG AAACTTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	--	---	---	TGTCCTAGGCCAGCCCTGCTTGCTCCTCGCTGTTATCTCAGTACTGCAAAAGAGAACACAGAC AT
ESTD- NFRMP	--	--	--	---	---	GGAGGAGGAGGTGGGAGGGGCTGCTGCTCCAGGTOCCACAGACAGAGAGGCGCTCAGTGG TATCCCAACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NFRAS	--	--	--	---	---	GTGTTTCTTAATCTTTTCCAGGAACACAGTGACCATAATCTTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGTTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTAACCTTGGCAATAGCATTGC ATCCCTGTGGTTTTTATAAAAAAT
ESTD-OTC	--	--	--	---	---	GTGACCTTCTCCTTAAACCTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAACAGAAAGGAGGATGTAAACA
ESTD-PAI1	--	--	--	---	---	GCCACCACACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCCC TCAGGGCACAGAGAGTCTGACACAGTGGGAGTCAGCCGTATCATCGGAGGCGCGGGCAC ATGGCAGGATGAGGGAAGACCAAGAGTCCTGTTGGGCCAAGTCTCTAGACAGACAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	CTCTTCAGGAACCACTGCTCTTACCAACACGACTTATTGCTGTCGAGAGGTACACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATCTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACTTTTCTGTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACITTAGGCTTCTGTATACCCATGCCC
ESTD- PBDA	--	--	--	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAATCTCTACCCGAGCTTGCTCGCATACAGAG GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	GGGGAGTAAACTTGGATTGGGAGATTTCAATTTCTACAGTGTCTGGTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCACTAGCCTATTCTGAGCCATATTAATTGGTTGTGCCCTTACAT ATTACTCTTGCCATTTCAAGAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTGGCACAGATTATCTTGTA
ESTD- PXMP1	--	--	--	---	---	ATGAAACATGGTCTTTTAAATTTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
ESTD- Per/RDS	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTG CTGGAGAAGAGCGTCCCGGAGAGCTGGAAGGCCT

ESTD-RDS	--	--	--	---	---	---	CCAGGGAATCTGAGAGCGAGCGAGGGCTGGCTGCTGGAGAAGAGCGTGCCGGAGACCTGGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGCAAGGCAAGGCAACAGGTGGAAGCCGAGGCGCAGACGACGAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACCT CCAAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- RYR1	--	--	---	---	---	---	CTTCGTGACGGGAGGTCACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACCGAGCGAGACTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAAATCAGCTGGAGTGGAGCCACTGCGCTGGGGCCAGGCCACT CCGAGTCGGGATGTCATACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	---	---	---	---	TGAACACCCCTGTGTCGGGAGCCAGGTTGTGTTCTCCTGGGAGCTGAGGAGTTGTTGTCTGTGTG CAGTCCCGCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACCTCTTTGGCCCGGAGAAGAC ATTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCCCTGTGGAAGACCCCAACCCCTGCCTCC CCACCCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	---	---	---	---	TTCACTTTGTGGATTGTTCTTTTGTCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTGTCTCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTCTGTA
ESTD-TAT	--	--	---	---	---	---	AAATGTGACGAGCCCTGATCCACAAGAGTGGTACCATTTCATCAGGGCCATCAGTTTCATTCAAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCACTTCATCTTAAATGACTTGTGGACAGGATCA ATTTCCCTCACCTAGAACGTTTGTTTACAAGTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THR8	--	--	---	---	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTCCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAAATCACAGGATCAGTTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD- TNFA	--	--	---	---	---	---	TTCTGCACTCTGTCTGGAAGTTAGAAGGAAACAGACCACAGCTGTGCCCAAAAGAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGTTTCAGCCTCCAGGTTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGTCCTCACTTCCAAATCCCGCCCGCCGGATGG
ESTD-TYR	--	--	---	---	---	---	TAGTGAAGTTTTTCATCTCTGTGAGCTTCTGGATTCTTGTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATGTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCTATGGGGATGACA

[illegible]

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EST11458 6	--	--	--	--	CCACTTTGGTAGTGGCAGTGTGACTCATCCACAATGATTCTCCAGTGTCTCATCTTGTTCGAGTTTT CTCTGCCATGTTGCTATTGCGAGGAGGACCTGTCCAGCAGATGATTACCATTTTCCACAGTGGT CCCATTAACAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	--	CGGTCTTCCTCCAGGTATTGTGCAGAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	--	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGCCATTGCGGCCCTCTCGGGGCCGTGG TCTCTGGTGTGGTAGTCTGGAGTCAAGGTGCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGTTCCCGCAGGTGCGATGGTCAACCCGACACAAAGGAGCGCGGTACCCCTGG CAATAT
EST36027 2	--	--	--	--	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTTCTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	--	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTTAGGATGAGGTGA TAGTAATGACCGATGGGGTCAGAACTGTTCTGTCCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCAGATC
EST78807 7	--	--	--	--	ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTGTCTCTCCAGGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAAGCCCGCAGGCACTGGGCTCCGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG
EST44438 3	--	--	--	--	GCAGCCAGGAGCCGCTGCACCATGCCCCGCATAGATGGGACCTCAAGCTGCACTTCAAGGACGTCT GCTCCGACCTAAGCGGAGAGCCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	--	--	--	--	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTGTCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAAGTATTACTGAGTAAGGGAAGTGAATGTTATTCAACTGG ATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTAGCTTAG
EST54419 8	--	--	--	--	CTTCTGCCCTAATTGATGATGTTGCTGTGGGACCTGAGCAGCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTGGGTTAGCGTGGTGTGTTGTTGTTACTA TAGTCCAAAGTGAA

EST10398	--	--	--	--	---	---	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTATGAAGGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTACATTTGGGGCTTGACTTTTCCAACACGGAGAAG CATTGTTTCTCGGGCCAAAGGATCTACCAATAGTGTCTATTAGGCATTG
EST36751	--	--	--	--	---	---	---	---	CCAAGTCGTTCAATTTTAGCTTTCGAGGTTTAACTCGATTACTTTTTCTATTCAAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	--	--	--	--	---	---	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCAATTAACAAATATTTACCTTTTGAANAATAAATG AAGGATTGACCTGCTTCGCTCTGGAAGAGATACCGTACCGTCTGACGTTTTTGAACAATACAGAT GCCTCCCTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288	--	--	--	--	---	---	---	---	GCCTCTATACCCCTGTGCTCCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTACAGGTTCAATGCAGGCTGTACAGGATGGAAGACTGCTGCTCCTGACGGGAGCCAGTGTGG ACAGACCCCTGGCTTTCAACACCTACGTCACCTTCCAAGTAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523	--	--	--	--	---	---	---	---	TTCCCGCAGCCCCCATCTTGGCAACCTGTGTCCTCAGGGGOCACCCCGGGGCACTCAACGCTCT CGCTCTCGGTAACATCCGGCGGGCGCGCTCTTGAAGCACATAGCTTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCGCGGGCTTGCCAGGGGOCAGCCCTGCAGAGAGAGGGGTCCCTGTGTGCT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707	--	--	--	--	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCCTAGAAGATACACGAGACCGA ATGTATCAAAATGGACATTACAGCAGGAACCTTCAACGATACCTGTCTGTGTAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGTGGACTCTTGCTGCTAAGAACCTT
EST74167	--	--	--	--	---	---	---	---	AGACATGAAGGAGTTGAAGGCTACAAATCGGAAGTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCAACGCTGTCCAAGGAGCTGACGGCGGCGAGGCGCGGCTGGCGCGGACATGGAGGA CGTGGCGGGCGCTGTGTGCAGTACCGCGGCGAGGTGCAGGCCCATGCTCGGCACAGACACCGAGGAGC TGCGGGTGGCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211	--	--	--	--	---	---	---	---	CGCTGGTGCAGTACCGGGGAGGTGCAGGCCATGCTCGGCCAGACGAGGAGCTCGCGGTGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGCTCTCCGCGATGCGGATGACCTGCAGAACGCGC TGCGAGTGTACAGGCGGGGCGCGAGGGGCGGAGCGGCTCAGCGCATCCGCGAGCGCTG GGGCCCTGTGTGAACAGGGCGGTGGGGCGCGCACTGTGGGCTC
EST36770	--	--	--	--	---	---	---	---	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGATCCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATACTCTTATTGGAAGGCCCTTAAGAAGGCTTATG

EST26021 1	---	---	---	---	TAATGTAAGCTCATCCACCAGAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCTCTGACGACCTTCACCTACCAAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTGCAACAAGACAAGCAAAAGCC
EST51212 0	---	---	---	---	ATCCTGAGCTCGCAATAAGCTTCTTGTTCTACTTCTCTCCACAAGCCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTCTCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	---	---	---	---	GTCCGAATCTCTCTGAAAGTGCCGGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGGACGGGCTCTCTGCGTGCATCTTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGGACGGGCTCTCTGCGTGCATCTTAAGCT CTGAGA
EST53018 6	---	---	---	---	ACAATCCAGGTCACACATTCAGAAAGAGGGGTTGTGCTGAGCCTGGGTAGGTCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	---	---	---	---	CTTCTATGGGATTTGACTTTATTTCTCATTTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAAGGAATAAATTCACAGTCAA AGAAACAAGCACTTTTCGAAACATTTGAAGTTGTTTGAACCTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	---	---	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGG ATCCAAAGGCCCACTCCCGAACCCTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	---	---	---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAATTTGGCTGGACTTGAGTCCCTGAACAGCAAGAGAAAGAGACCCCGAGAAAT CACAGTGGGCACGTGCGTCTACGGCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082 --	---	---	---	---	TCAGGGTGGCTGGACCCAGGCCCCAGCTCTGCAGAGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGGCCAGGGGCCCAAGGAGGGCACCTGGCTTACGCTGCTCAGCCCTGCTGTGCAC CCAGATCACTGTCTCTGOCATGGCCCTGTGGATGCGCTCTGCCCCCTCTGCGGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGGG
EST45311 0	---	---	---	---	GGCCTCCTCTCTCCAAATTTGTCCCTATAGTTTCCCTATTAAAGTGAACATACATTCATCTTTAGT GGATAGATGCACACAACACACAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCATTTAACAGCCCTTATTCATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGTAAT

EST65258 8	--	---	---	---	---	TGCCCCATCACGGCGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTACCAATTAACCAGAAAT CCAGTTATTTCCACCCTCAAAATGACAGCCATGGCGCGGGTCTCTGGGGCTCGTCGGGGGG ACAGTCCACTCTGACTGGCAGACTCTTTGCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGTGAG GTTAGGTCGTGTTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	--	---	---	---	---	ATGACGGATGAAGGTGGACAGGGGAGGAGAGGGCCAACTGTGCATCCAGGGCTGCAGATGTCGCTG GACTATGGGTTTGTACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTAATAGCATTTGTTTAGCATTACCTAA TTTTTTCTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTGGTTTTGAACTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGGTGCATGCA
EST35879 9	--	---	---	---	---	GAGATCGGTGTGAGTTATTAGGCATGGTTACCTGTGATCTCCCAATCTTGCGGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5	--	---	---	---	---	GGAAAGAGATTTAAGAAGCTTGATTTGGACAATCTGTTCTTTGAGTGTGGAAGATTCATGTCTCT GCCTGAGTTACAACAGAACTCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045 6	--	---	---	---	---	GGAAATTAATAAATATTTTAAATACCTCCATTTTGCTTATCCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTGATGTGGCAATTTGTTTCTTACAAAATCGGATGGAAATCT GTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
EST52908 0	--	---	---	---	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTCTGCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590	--	---	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTGGGCTCAGGAT GCCGGAAAAATGAC
EST76136	--	---	---	---	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	--	---	---	---	---	CTCTGGATGGGTTACAGGTGGCAGGCCACAAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACATGGCGGGGATGGCGGGGAGTCTGCTGGT TGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT TGGCCAAGGAGGGGGGGTGGCCATGCCCTGAGATGTAGATGGCGGC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence						



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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

## WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.

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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12Q 1/68, C12N 15/11</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 98/20165</b> <b>(43) International Publication Date:</b> 14 May 1998 (14.05.98)
<b>(21) International Application Number:</b> PCT/US97/20313 <b>(22) International Filing Date:</b> 5 November 1997 (05.11.97)  <b>(30) Priority Data:</b> 60/030,455      6 November 1996 (06.11.96)      US  <b>(71) Applicant (for all designated States except US):</b> WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).  <b>(74) Agents:</b> GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>  <b>(88) Date of publication of the international search report:</b> 12 November 1998 (12.11.98)
<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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# INTERNATIONAL SEARCH REPORT

International Application No

PL 1/US 97/20313

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 C12Q1/68 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract	1-20

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

23.09.1998

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## INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10  emb1  Accession number: hst27766, 12 January 1995  ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence"  XP002067789  * Sequence *</p>	1-3,10, 11
X	<p>SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING"  AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638  see abstract  see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1  see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3, 7-10,13, 14,17-20
X	<p>FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996  see abstract  see page 1, line 5 - page 2, line 17  see page 9, line 9 - page 10, line 15;  tables 2,3</p>	1-3,7-9, 17-20
X	<p>HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION"  AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114  see the whole document</p>	10-16, 18-20
X	<p>GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS"  NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290  see the whole document</p>	18-20

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# INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document</p> <p style="text-align: center;">-----</p>	18-20

# INTERNATIONAL SEARCH REPORT

L national application No.  
PCT/US 97/20313

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  


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4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2269 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

## INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC/US 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A	23-05-95
		CA 2175695 A	11-05-95
		EP 0726905 A	21-08-96
		US 5762876 A	09-06-98
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FR 2722295 A	12-01-96	NONE	
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